

GenCore version 4.5
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OM protein - protein search, using SW model

Run on: August 21, 2002, 15:43:08 Search time 17.84 Seconds

(without alignments) 1842 071 Million cell updates/sec

File: US-09-780-576-2

Perfect score: 1778

Sequence: 1 MQAVDNLISADGNISLCTRD.....SQDNKKKKQDGDNEETPM 342

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 98

Maximum Match 100%

Listing first 45 summaries

Database: 1: PIR1:
2: PIR2:
3: PIR3:
4: PIR4:

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	394	22.2	342	2	A40191 platelet activating factor receptor
2	392.5	22.1	342	2	platelet activating factor receptor
3	379.5	21.3	341	2	B45680 G protein-coupled
4	366	20.6	341	2	platelet activating factor receptor
5	362	20.4	341	2	platelet activating factor receptor
6	357.5	20.1	308	2	150241 G protein-coupled
7	349	19.1	359	2	S15403 angiotensin II receptor
8	344	18.5	344	2	T09408 angiotensin II receptor
9	329	18.0	344	2	T09408 angiotensin II receptor
10	326	18.3	359	2	S44425 angiotensin II receptor
11	325.5	18.3	359	2	148705 angiotensin II receptor
12	325	18.3	359	2	A48657 angiotensin II receptor
13	321	18.1	359	2	T01104 angiotensin II receptor
14	319	17.9	359	2	A42656 heptahelical P2Y5
15	319	17.9	359	2	A42656 angiotensin II receptor
16	319	17.9	359	2	A42656 angiotensin II receptor
17	318	17.9	359	2	J01194 angiotensin II receptor
18	318	17.9	359	2	J01194 angiotensin II receptor
19	317.5	17.9	359	2	S08208 angiotensin II receptor
20	317.5	17.9	359	2	S08208 angiotensin II receptor
21	314.5	17.7	359	2	156504 mu opiate receptor
22	314	17.7	359	2	J01516 angiotensin II receptor
23	313.5	17.6	388	2	138435 angiotensin II receptor
24	313.5	17.6	388	2	J01694 angiotensin II receptor
25	309	17.4	400	2	S65553 mu opiate receptor
26	309	17.4	400	2	S65553 mu opiate receptor
27	306	17.2	397	2	S66518 proteinase activator
28	304.5	17.1	398	2	A57510 mu opiate receptor
29	299	16.8	388	2	J02434 kappa opiate receptor

ALIGNMENTS

RESULT 1

A40191

platelet activating factor receptor - human

C:Species: Homo sapiens (man)

C:Date: 28-Aug-1992 #sequence_revision 28 Aug 1992 #text_change 20 Jun 2000

C:Accession: A40191; J00479; J01769; J01769; A42841; J01923

R:Kunz, D.; Gerard, N.P.; Gerard, C.

J. Biol. Chem. 267, 9101-9106, 1992

A:Title: The human leukocyte platelet activating factor receptor: cDNA cloning, cell

A:Reference number: A40191; M01D:92250505

A:Accession: A40191

A:Molecule type: mRNA

A:Residues: 1-342 <N>

A:Cross-references: GR-M76674; NID-9456293; PIDN-AAA60002; PID-9456294

R:Yee, R.D.; Prossnitz, F.R.; Zou, A.; Cochrane, C.G.

Biochem Biophys Res Commun 190, 105-111, 1991

A:Title: Characterization of a human cDNA that encodes a functional receptor for platelet activating factor

A:Reference number: J00479; M01D:92028922

A:Accession: J00479

A:Molecule type: mRNA

A:Residues: 1-342 <N>

A:Cross-references: GR-M00436; NID-9189547; PIDN-AAA60001; PID-9189548

A:Experimental source: granulocyte, cell line HL 60 all

R:Nakamura, M.; Honda, S.; Izumi, T.; Sakonaka, C.; Mutoh, H.; Minami, M.; Bito, H.;

J. Biol. Chem. 266, 20400-20405, 1991

A:Title: Molecular cloning and expression of platelet activating factor receptor from

A:Reference number: A40191; M01D:92041873

A:Accession: A40191

A:Molecule type: mRNA

A:Residues: 1-342 <N>

A:Cross-references: GR-M00436; NID-9219975; PIDN-AAA60002; PID-9219976

R:Soumireu, T.; Tsuchimochi, H.; McGovern, C.G.A.; Mutoh, H.; Shimizu, I.; Kurachi, Y.

Biochem Biophys Res Commun 189, 617-624, 1992

A:Title: Molecular cloning and characterization of the platelet activating factor

A:Reference number: J01359; M01D:93112021

A:Accession: J01359

A:Molecule type: mRNA

A:Residues: 1-315, 'N', 317-342 <N>

A:Experimental source: heart

R:Sevitt, C.E.; Schwickerath, V.L.; Gdalska, R.; Gray, P.W.

Genomics 13, 833-834, 1992

A:Title: The human platelet-activating factor receptor gene (PTAFR) contains no intron

A:Reference number: A42831; M01D:92347886

A:Accession: A42831

A:Molecule type: DNA

A:Residues: 1-226, TG, 229-342 <N>

A:Cross-references: GR-M00436; NID-9189547; PIDN-AAA60002; PID-9189548

R:Chao, P.H.; Halonen, M.; Regan, J.W.

Am. J. Respir. Cell Mol. Biol. 8, 240-244, 1993

Active cloning of a human platelet activating factor receptor gene: evidence for an in

Accession number: F51923; MIM:93192035

Accession: F51923

Status: preliminary; translated from CH/IMH/IDHJ

Molecule type: DNA

Accession: F51923

Accession: F51923; GB: S6396; NID: 4298580; PID: A05755.1; PID: 4298581

Accession: F51923

Accession: F51923

Accession: F51923; GB: S6396; NID: 4298580; PID: A05755.1; PID: 4298581

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Accession: F51923

Accession: F51923

Accession: F51923

Db 292 FTVCLMNFNCMDPTFYFAKGYKFFKFMMLK.FGVSVSSVAKSAPEENSPEMTETG 350

QY 342 M 342

Db 351 M 351

RESULT 4
S63666
Platelet activating factor receptor mouse

C:Species: Mus musculus (house mouse)

C:Date: 28-Jul-1996 #sequence_revision 13 Mar-1997 #text_change 28-Jun-2000

C:Accession: S63666

R:Shimizu, S.; Matsuda, Y.; Nakamura, M.; Waga, I.; Kume, K.; Izumi, T.; Shimizu, T.

Biochem. J. 314: 671-678, 1996

Attribute: A murine platelet activating factor receptor gene: cloning, chromosomal localization

A:Reference number: S63666; MUID:96239129

A:Accession: S63666

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-341 <ISH>

A:Cross-references: EMBL:050872, NID:q1256324, PDB:AA03408.1, PIR:q1256925

A:Superfamily: ATP receptor P2U

Query Match

Best Local Similarity 20.6%; Score 366; DB 2; Length 341;

Matches 96; Conservative 64; Mismatches 133; Indels 28; Gaps 10;

QY 20 DYKTIQVLFELTYLVFVGLITNGLAMKIFPI--RKSNTF--TELKNTVISLMLLT 76

Db 10 DSEFRITLPIVSVIFELVANGVGLVFAVLYESKRLNEIKIIVMLIMDLLEFLIT 69

QY 77 FPKKILSDAKLIGGPRITFCVQVSVIFEFYVYISIPGLITIDRYOKTRPRTSNRK 136

Db 70 LPLMTVY 129

QY 137 NLGAKILSVIIVAM--FLSLPMLLNKQPRKVRKVSFLKSEF--LVME 184

Db 130 TRRGKISLILVSIIVAIASVFLATISTNLVYNKDSGNTTCHPHIVSVPIIVAVH 189

QY 189 IVVYICQVITWIMFLI-VIVGYTLIKELRYSVPTKRVKRVKRVKRVKRVKRVKRV 247

Db 190 FIVEFELVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLV 243

QY 248 GCVPHFAPRIVTISQFVFCVFCVFCVFCVFCVFCVFCVFCVFCVFCVFCVFCVFC 307

Db 244 GCVPHIVVQVPLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLV 301

QY 308 -----SLISMCKPNSATS 321

Db 302 HISEKFSYMSKRSKRSKRSKRSKRSKRSKRSKRSKRSKRSKRSKRSKRSKRSKRS 321

RESULT 5

S43252

Platelet-activating factor receptor rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 20-Jul-1994 #sequence_revision 13 Nov 1996 #text_change 24 Nov 1999

C:Accession: S43252

R:Ridder, H.; Honda, Z.; Nakamura, M.; Shimizu, T.

Biochem. J. 297: 21-21R, 1994

Attribute: Cloning, expression and tissue distribution of rat platelet activating factor

A:Reference number: S43252; MUID:94222063

A:Accession: S43252

A:Molecule type: mRNA

A:Residues: 1-341 <RIT>

A:Cross-references: GR:04740; NID:q470384; PDB:AAAI8422.1; PIR:q470385

A:Superfamily: ATP receptor P2U

Query Match

Best Local Similarity 20.4%; Score 362; DB 2; Length 341;

Matches 96; Conservative 64; Mismatches 133; Indels 28; Gaps 10;

QY 20 DYKTIQVLFELTYLVFVGLITNGLAMKIFPI--RKSNTF--TELKNTVISLMLLT 76

Db 10 DSEFRITLPIVSVIFELVANGVGLVFAVLYESKRLNEIKIIVMLIMDLLEFLIT 69

QY 77 FPKKILSDAKLIGGPRITFCVQVSVIFEFYVYISIPGLITIDRYOKTRPRTSNRK 136

Db 70 LPLMTVY 129

QY 137 NLGAKILSVIIVAM--FLSLPMLLNKQPRKVRKVSFLKSEF--LVME 184

Db 130 TRRGKISLILVSIIVAIASVFLATISTNLVYNKDSGNTTCHPHIVSVPIIVAVH 189

QY 189 IVVYICQVITWIMFLI-VIVGYTLIKELRYSVPTKRVKRVKRVKRVKRVKRVKRV 247

Db 190 FIVEFELVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLV 243

QY 248 GCVPHFAPRIVTISQFVFCVFCVFCVFCVFCVFCVFCVFCVFCVFCVFCVFCVFC 307

Db 244 GCVPHIVVQVPLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLV 301

QY 308 -----SLISMCKPNSATS 321

Db 302 HISEKFSYMSKRSKRSKRSKRSKRSKRSKRSKRSKRSKRSKRSKRSKRSKRSKRS 321

Matches 96; Conservative 66; Mismatches 120; Indels 50; Gaps 10;

QY 20 DYKTIQVLFELTYLVFVGLITNGLAMKIF--FQIRSKSNFIIPIKNIIVISLMLLT 76

Db 10 DSEFRITLPIVSVIFELVANGVGLVFAVLYESKRLNEIKIIVMLIMDLLEFLIT 69

QY 77 FPKKILSDAKLIGGPRITFCVQVSVIFEFYVYISIPGLITIDRYOKTRPRTSNRK 136

Db 70 LPLMTVY 129

QY 137 NLGAKILSVIIVAM--FLSLPMLLNKQPRKVRKVSFLKSEF--LVME 184

Db 130 TRRGKISLILVSIIVAIASVFLATISTNLVYNKDSGNTTCHPHIVSVPIIVAVH 189

QY 177 FPKSEFGLVY 236

Db 190 FPKSEFGLVY 233

QY 247 KVFITIAVFFTCVFPFAPRIVTISQFVFCVFCVFCVFCVFCVFCVFCVFCVFCVFCVFCVFCVFC 296

Db 234 -VCVIAVAVVFCVPHVAVVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLV 290

QY 297 IYFPICKSPRN--SLISMCKPNSATS 321

Db 291 IYFPICKSPRN--SLISMCKPNSATS 321

RESULT 6

150241

G protein-coupled receptor 6H1 - chicken

N:Alternate names: purinoceptor 6H1

C:Species: Gallus gallus (chicken)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 02 Jun 2000

C:Accession: 150241; J04618

R:Kaplan, M.H.; Smith, D.L.; Sundick, R.S.

J. Immunol. 151, 628-636, 1993

Attribute: Identification of a G protein-coupled receptor induced in activated T cells

A:Reference number: 150241; MUID:9424058

A:Accession: 150241

A:Molecule type: mRNA

A:Residues: 1-308 <KAP>

A:Cross-references: GR:06109; NID:q304383; PDB:AAH0587.1; PIR:q304384

A:Webb, T.E.; Kaplan, M.H.; Barnard, E.A.

Biochem. Biophys. Res. Commun. 219, 105-110, 1996

Attribute: Identification of 6H1 as a P2Y purinoceptor. 1235

A:Reference number: J04618; MUID:96190677

A:Accession: J04618

A:Molecule type: mRNA

A:Residues: 1-308 <WEB>

A:Cross-references: GR:06109; NID:q304383; PDB:AAH0587.1; PIR:q304384

A:Experimental source: T-cells

C:Comment: This receptor plays a role in T-cell activation.

C:Genetics:

A:Gene: P2Y5

C:Superfamily: ATP receptor P2U

C:Keywords: G protein coupled receptor; transmembrane protein

F:15-40/Domain: transmembrane #status predicted <TM>

F:51-74/Domain: transmembrane #status predicted <TM>

F:89-109/Domain: transmembrane #status predicted <TM>

F:113-157/Domain: transmembrane #status predicted <TM>

F:177-207/Domain: transmembrane #status predicted <TM>

F:227-248/Domain: transmembrane #status predicted <TM>

F:269-292/Domain: transmembrane #status predicted <TM>

Query Match

Best Local Similarity 20.1%; Score 357.5; DB 2; Length 308;

Matches 87; Conservative 68; Mismatches 125; Indels 15; Gaps 8;

QY 14 TSLCTHDKYITQVLFELTYLVFVGLITNGLAMKIF--FQIRSKSNFIIPIKNIIVISLMLLT 72

Db 3 SSNCSTELSEKRTLYGVFSMVAVLLANVAIIFFTLKVRNRETTVMNLNLSLL 62

QY 145 SVVIAWAFMLTSLPMLITN RQPRDKVKKCSF LKSEFGVMEIYNTQ 195
 DB 149 CIIIMLAGLASLPIIHNNVFITENTITVCAPHEHNSNTLIGIGITNNIHS--C- 205
 QY 196 VIFWNIPLIVCYITLTKELKRSVVRIGCVKVRKKVNAVPIIAVPIICVPPHA 255
 DB 206 ---FFFLITLSTYLLMKLKKAVFIQK---NNPRNDITPITMAIVLFFP-----FS 262
 QY 256 RIVYHLSQIRDFV-----DCTAENTLFFYKESLMTLSINACIDPIYFPCCKSPNS 308
 DB 254 WIPDQIFPIFIVLIGQGITSPGRIADIVDAMPITITWIAVFNNTNIPYPCCKKKKK 312
 QY 309 LISMK-CENSAISLSQPNK 328
 DB 313 IIOQLKYLPPAKKSHSNLSIK 333

RESULT 10

S44425
 angiotensin II receptor type 1 - dog
 C.Species: Canis lupus familiaris (dog)
 C.Date: 19-Mar-1997 #sequence_revision 19 Mar-1997 #text_change 24-Nov-1999
 C.Accession: S44425
 R.Burns, L.; Clark, K.L.; Bradley, J.; Robertson, M.J.; Clark, A.J.L.
 FEBS Lett. 343, 146-150, 1994
 A.Title: Molecular cloning of the canine angiotensin II receptor. An AT1-like receptor
 A.Reference number: S44425, MIMD:94222188
 A.Accession: S44425
 A>Status: nucleic acid sequence not shown
 A.Molecule type: mRNA
 A.Residues: 1-359 <DB>
 A.Cross-references: PDB:1AB30674.1; PDB:0546569
 A.Experimental source: liver
 C.Superfamily: vertebrate rhodopsin

Query Match

18.3% Score 326, DB 2, Length 359,
 Best Local Similarity 29.2%, Pred. No. 1.5e-20,

Matches 92; Conservative 54; Mismatches 147; Indels 22; Gaps 8;

QY 26 VLEPIIATVLEFVGLITNGI-AMRIIPQIRSKNFIPIKNTVISDLMITPPKILSD 84
 DB 29 VMPIFLKSTITVAVITFNSLVTVIYFIMKLTVA SVLLNLALDLFLITIPWAVYT 88
 QY 85 AKICGPIPLTFVCGVTSVIFVFWTISISPLGLITIDRYQKTRPKTSNKNLGAAL 144
 DB 89 AMEYRMPGNTICKIASASVFNIVASVFLITLISURVAVIAPHKSHVPRIMIAKVT 148
 QY 145 SVVIAWAFMLTSLPMLITN RQPRDKVKKCSF-----LKSEFGVMEIYNTQ 195
 DB 149 CIIIMLAGLASLPIIHNNVFITENTITVCAPHEHNSNTLIGIGITNNIHS--C- 205
 QY 196 VIFWNIPLIVCYITLTKELKRSVVRIGCVKVRKKVNAVPIIAVPIICVPPHA 255
 DB 206 ---FFFLITLSTYLLMKLKKAVFIQK---NNPRNDITPITMAIVLFFP-----FS 262
 QY 256 RIVYHLSQIRDFV-----DCTAENTLFFYKESLMTLSINACIDPIYFPCCKSPNS 308
 DB 254 WIPDQIFPIFIVLIGQGITSPGRIADIVDAMPITITWIAVFNNTNIPYPCCKKKKK 312
 QY 309 LISMK-CENSAISLSQPNK 328
 DB 313 IIOQLKYLPPAKKSHSNLSIK 333

RESULT 11

S44705
 proteinase activated receptor 2 - mouse
 C.Species: Mus musculus (house mouse)
 C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Nov-1999
 C.Accession: S44705
 R.Nystedt, S.; Larsson, A.K.; Aberq, B.; Sundelin, J.
 J. Biol. Chem. 270, 5950-5955, 1995

A.Title: The mouse proteinase-activated receptor 2 cDNA and protein. Molecular cloning a
 A.Reference number: S44705, MIMD:95157620
 A.Accession: S44705
 A>Status: preliminary, translated from Gh/Fmh/70004
 A.Molecule type: mRNA
 A.Residues: 1-399 <DB>
 A.Cross-references: EMBL:248043; NID:9661020; PDB:1AAB9007.1; PDB:1A6021
 C.Superfamily: ATP receptor P2u

Query Match

18.3% Score 325.5, DB 2, Length 399,
 Best Local Similarity 27.6%, Pred. No. 1.5e-20,

Matches 92; Conservative 74; Mismatches 141; Indels 27; Gaps 12;

QY 22 KIQVIFPLIVCYITLTKELKRSVVRIGCVKVRKKVNAVPIIAVPIICVPPHA 80
 DB 74 KITTVI PVVYIIVFVGLISNMAIPIIPPKKKPAVIMANIALADLSVIMPIIK 133
 QY 81 ILSDAKLGITPLTFVCGVTSVIFVFWTISISPLGLITIDRYQKTRPKTSNKNLGA 140
 DB 134 ISYHAGNNVYGCALCKVLIGFYGNMYSILPMGLISQRYVAVINPM-CHPRKKAN 191
 QY 141 AKI-LSVIAWAFMLTSLPMLITN RQPRDKVKKCSF LKSEFGVMEIYNTQ 196
 DB 192 IAVGSLAMILLFLVITIPYVMKQIYIPA-LNITTCGVDEEVLV-GDMNPFSLA 249
 QY 197 ---IFWNIPLIVCYITLTKELKRSVVRIGCVKVRKKVNAVPIIAVPIICVPPHA 254
 DB 250 IGVFLPALLITASAVVIMIKLRSSAMDESEK--KORARILIVIAVPIICFALSN 307
 QY 255 AK-IPVILSLTRVEDCTAENTLFFYKESLMTLSINACIDPIYFPCCKSPNS 308
 DB 308 LIAVHYPLIKFO-----RQSHVAVIIVALICISLNSCIDPEYVYVSKDFRHMAL 361
 QY 314 KCPNSAT-----SLSDNKKKKGQDPNRET 340
 DB 362 LTPSVRTVNMQITSL-SNKPFRKSISYSSNST 393

RESULT 12

A48857

angiotensin II receptor type 1 - rabbit
 C.Species: Oryctolagus cuniculus (domestic rabbit)
 C.Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
 C.Accession: A48857
 R.Burns, K.D.; Inagami, T.; Harris, R.C.
 Am. J. Physiol. 264, F645-F654, 1993
 A.Title: Cloning of a rabbit kidney cortex AT1 angiotensin II receptor that is presen
 A.Reference number: A48857; MIMD:93236091
 A.Accession: A48857
 A>Status: preliminary
 A.Molecule type: nucleic acid
 A.Residues: 1-359 <DB>
 A.Cross-references: GR:559041; NID:9296614; PDB:1AAR2339.1; PDB:1299615
 A.Note: sequence extracted from NCB1 tubule cells
 C.Superfamily: vertebrate rhodopsin
 C.Keywords: G protein coupled receptor; transmembrane protein

Query Match

18.3% Score 325, DB 2, Length 359,
 Best Local Similarity 29.2%, Pred. No. 1.5e-20,

Matches 92; Conservative 55; Mismatches 146; Indels 22; Gaps 8;

QY 26 VLEPIIATVLEFVGLITNGI-AMRIIPQIRSKNFIPIKNTVISDLMITPPKILSD 84
 DB 29 VMPIFLKSTITVAVITFNSLVTVIYFIMKLTVA SVLLNLALDLFLITIPWAVYT 88
 QY 85 AKICGPIPLTFVCGVTSVIFVFWTISISPLGLITIDRYQKTRPKTSNKNLGAAL 144
 DB 89 AMEYRMPGNTICKIASASVFNIVASVFLITLISURVAVIAPHKSHVPRIMIAKVT 148
 QY 145 SVVIAWAFMLTSLPMLITN RQPRDKVKKCSF-----LKSEFGVMEIYNTQ 195

DB 149 CIIIMLALASLAIPIHRNVFTEHNINIVCAHYESQNSLITIGLIT-KNIIIGPL- 205
 QY 149 VIFWNIIVIVYITITITELYSVRLVWVYVPRKKVNVKVI-ILAVFIVFPIIF 254
 DB 206 FFFIIILSYLLIMKALPKAVELK-NKPNRNDIKFIMAVLIPFSWVQI 258
 QY 256 AMRYEINOTRIYVQVIAINILFYKESIMLSINAGIDPFFPLCKSPKNSLSMLK 314
 DB 256 FFFIIVLIVGLAVIIEKRLADIVDIAMPITITIAVFNNINLEFYGLFKKKKKFELDLK 318
 QY 313 CPNSATSLSDNKR 328
 DB 313 YIFPKAKSHSNLSK 333

RESULT 14

Angiotensin II receptor type 1 human

Accession number: angiotensin II receptor 1A

Species: Homo sapiens (man)

Cloned by Oct 1992 #sequence revision 05-Sep-1997 #text change 21-Jul-2000

Accession: J01104; J01402; J00574; J00267; A44014; S18083

Biocchem Biophys Res Commun 186: 277-284, 1992

At title: Cloning, expression, and characterization of a gene encoding the human angiotensin II receptor

Accession number: J01104; M01092337608

Accession: J01104

Molecule type: DNA

Accession: J01104

Accession: J01104

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Accession: J01104

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Accession: J01104

F:65-90/Domain: transmembrane #status predicted <TM>
 F:103-124/Domain: transmembrane #status predicted <TM>
 F:145-167/Domain: transmembrane #status predicted <TM>
 F:194-215/Domain: transmembrane #status predicted <TM>
 F:241-264/Domain: transmembrane #status predicted <TM>
 F:261-305/Domain: transmembrane #status predicted <TM>
 F:4176-188/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.1% Score 321 DB 2 Length 459

Best Local Similarity 28.7% Pred. No. 436-207

Matches 92 Conservative 56 Mismatches 139 Indels 14 Gaps 9

QY 26 VIFWNIIVIVYITITITELYSVRLVWVYVPRKKVNVKVI-ILAVFIVFPIIF 84
 DB 29 VIFWNIIVIVYITITITELYSVRLVWVYVPRKKVNVKVI-ILAVFIVFPIIF 88
 QY 85 AKIQTGPIRTVCOVTSVIFVYIMYISISPIGLIIDRYOKTRPKYSNPKNLCAKIL 144
 DB 89 AMRYEINOTRIYVQVIAINILFYKESIMLSINAGIDPFFPLCKSPKNSLSMLK 148
 QY 145 SVIVIAFVELLSLEKMLIN-FOPEKKVKKKSF-----LKSGLVWHLIVYICQ 195
 DB 149 CIIIMLALASLAIPIHRNVFTEHNINIVCAHYESQNSLITIGLIT-KNIIIGPL- 205
 QY 196 VIFWNIIVIVYITITITELYSVRLVWVYVPRKKVNVKVI-ILAVFIVFPIIF 254
 DB 206 FFFIIILSYLLIMKALPKAVELK-NKPNRNDIKFIMAVLIPFSWVQI 258
 QY 256 AMRYEINOTRIYVQVIAINILFYKESIMLSINAGIDPFFPLCKSPKNSLSMLK 314
 DB 256 FFFIIVLIVGLAVIIEKRLADIVDIAMPITITIAVFNNINLEFYGLFKKKKKFELDLK 318
 QY 309 LISMLK-CPNSATSLSDNKR 328
 DB 313 YIFPKAKSHSNLSK 333

RESULT 14

heptahelical P2Y5-like receptor - human

Accession: J05549

Accession: J05549

Accession: J05549

Accession: J05549

Accession: J05549

Accession: J05549

Accession: J05549

Accession: J05549

Accession: J05549

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Accession: J05549

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Accession: J05549

Accession: J05549

Accession: J05549

Accession: J05549

Accession: J05549

Accession: J05549

Accession: J05549

Accession: J05549

Accession: J05549

Job time: 158 sec

DB 194 KRWKLYLSTIIIFIEVVGFIPLLNWSSVYRLRPATLSQIGTN-----KKV 247
QY 235 NKKVFIHIAVFICFVPEHFAHIFVTHSOTRDVDCIAENTLIPYVKSTIMLSLACID 294
DB 248 LKMTIVMAFVFCFVNSVLFYALVKSQALINCHERPAKIMPTICLATINCPD 307
QY 295 PTVEFLCKSFERN 308
DB 308 PTVEFLCKSFERN 321

RESULT 15

A42656
angiotensin II receptor type 1B (AT1) - rat
N:Alternate names: angiotensin II receptor chain B
C:Species: Rattus norvegicus (Norway rat)
C:date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C:Accession: A42656; S20423
R:Sandberg, K.; H., H.; Clark, A. I.; Shapira, H.; Galt, K.J.
J. Biol. Chem. 267, 9455-9458, 1992
A:title: Cloning and expression of a novel angiotensin II receptor subtype.
A:Reference number: A42656; M01D:92250585
A:Accession: A42656
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <SAS>
A:Cross-references: GR:M00065; NID:q202801; PDB:AAA40704.1; PDB:q202802
A:Experimental source: adrenal cortex
A:Note: sequence extracted from NCH1 backbone (NCHIN:100262, NCHIP:100268)
R:Wai, N.; Inagami, T.
FEBS Lett. 298, 257-260, 1992
A:title: Identification of two subtypes in the rat type I angiotensin II receptor.
A:Reference number: S20423 M01D:92183879
A:Accession: S20423
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-459 <TMS>
A:Cross-references: GB:X64052; NID:q57521; PDB:CAA45410.1; PDB:q57522
A:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 17 98; Score 319; DB 2; Length 359;
Best Local Similarity 29.68; Pred. No. 4.9e-20;
Matches 92; Conservative 54; Mismatches 137; Indels 28; Gaps 10;
QY 26 VLPPLATVLPFVGLIINCL-AMRIPOIRSKSNFIFLKNIVISDLMITPPFKIISD 84
DB 29 VMPTLELSIFVVGIFGNSLVIVFYMKLTVASVELLMALADLCFLTLPMAVYT 88
QY 85 AKIGTGLRIFVCOVSVIFFTNYISIPGLITIDRYOQTRPRKISNPKNIGAKIL 144
DB 89 AMFYRWPPGNHICKIASASVSFNIVASVPLITCISIDRYLAIVHPKSRIRRTIMIAKVP 148
QY 145 SVVIAWMPFLISTPNMILTRNQ-PRGNVKKRSP-----LKSEGLWHEIVNYIQ 195
DB 149 CIIIMLMAGIASIPAVYIRNVYFIENTINITYCAHYRSONSTLPICGLIT-KNIIQV-- 205
QY 196 VIVMNFILIVCYTLLIKELYSVYRFGVGRPKRVNKKV-ILIAV--FPICFVP 251
DB 206 ---FFPLIITSTYLIMKALKKAYKTK--NTPR---NDIFRITIMIVLEFFFSWVP 255
QY 252 PFRFAKITVTTISQTDVDCIAENTLIPYVKSTIMLSLACIDPPIYFLCKSFERNLS 311
DB 256 HQIFTEFLVILQIGIIRDCIADIVIPAMPTICIAVFNNCLNIPFYGLCKKKKKYPIQ 315
QY 312 MLK-CPNSATS 321
DB 316 LKATIPPAKS 326

Search completed: August 21, 2002, 15:45:46



81. **RECTOR, J.**
 82. **MOL. PHARMACOL.**, 60:432-439(2001).
 83. **EMBL**: AF314449; **AAK0944.1**.
 84. **EMBL**: AF318115; **AAK0944.1**.
 85. **EMBL**: AB052644; **BAB0084.1**.
 86. **LOCUS**: 198000276; **CH2K_Rhodosp.**
 87. **PLASMID**: pF0001.7fm.1.1
 88. **PROTEIN**: P000247; **CH2K_Rhodosp.**
 89. **PROSITE**: PS02621; **G PROTEIN-RECEP.F.1.2**. 1.
 90. **SEQUENCE**: 442 AA; 394 kD MW; 85540274608917650 CDS64;

[illegible]

RESULT	2	098718	
110	098718	FREELIMINARY:	PRT: 342 AA.
111	098718		
112	01-JUN-2001	(TREMBLER, 17, created)	
113	01-JUN-2001	(TREMBLER, 17, last sequence update)	
114	01-OCT-2001	(TREMBLER, 19, last annotation update)	
115	HYPOPHYSICAL_49.5_KDA_PROTEIN.		
116	Macaca fascicularis (Crab-eating macaque) (Cynomolgus monkey).		
117	Endometrial; Choroida; Craniola; Vertebral; Endosteostomi;		
118	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;		
119	Cercopithecoidea; Macaca.		
120	NCBI TaxID: 95411.		
121			
122	SEQUENCE FROM N.A.		
123	TISSUE: Frontal Lobe Left.		
124	Osada N., Hida M., Kusuda T., Tanuma R., Iseki K., Hirai M., Terao K.,		
125	Suzuki Y., Saitano S., Hashimoto K.?		
126	Isolation of full length cDNA clones from macaque brain cDNA		
127	library.		
128	Submitted (FEF 2001) to the EMBL/GenBank/DDBJ databases		
129	EMBL: AB056485; FAF48404.1.		
130	InterPro: IPR000276; cdkc_RhoGAP.		
131	PIRfam: PF00001; 7tm_1_1.		
132	PRINTS: PR00247; cdkc_RhoGAP.		
133	PROSITE: PS05062; G_PROTEIN_RECEP_F1_2; 1.		
134	Hypothetical protein.		
135	SEQUENCE: 342 AA; 39437 MW; 4021BF987FCC48599 CRC64;		

Best Local Similarity 98.08; Pred. No. 166-148;
Matches 335; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY	1	MOAYVNIISAKENISITCTHOKYICQVAFPELYATVAFVGLITNLSAMRPFEDJPKSNTI	60
Db	1	MOAIIINISAGONISCTHOKYICQVAFPELYATVAFVGLITNLSAMRPFEDJPKSNTI	60
QY	61	IFLKNTVTSIDLMITFPPKITSDAKIGTGPRIHVQVTSVIFEFYTMYSISPIGLIIT	120
Db	61	IFLKNTVTSIDLMITFPPKITSDAKIGTGPRIHVQVTSVIFEFYTMYSISPIGLIIT	120
QY	121	DBYQCTTRPFRKISNKKNLIGAKIISVLIWAFMFIISLNMILINOPRIKRNKCSPIKS	180
Db	121	DBYQCTTRPFRKISNKKNLIGAKIISVLIWAFMFIISLNMILINOPRIKRNKCSPIKS	180
QY	181	FFGLIWMHFIVNVTUVIPIWINFIVVYTLITKELYSYSTVTPVAVYVPPKRVNYPVT	240
Db	181	FFGLIWMHFIVNVTUVIPIWINFIVVYTLITKELYSYSTVTPVAVYVPPKRVNYPVT	240
QY	241	IAVEFICGVPRPHARIPYTLISQTRDVEFCSTENILIFYUKESITMISTINACIDBPITYF	300
Db	241	IAVEFICGVPRPHARIPYTLISQTRDVEFCSTENILIFYUKESITMISTINACIDBPITYF	300
QY	301	ICKSPFNLSLSMLKCPNSATSIISONRRKKRQOCPDNPETPM	362
Db	301	ICKSPFNLSLSMLKCPNSATSIISONRRKKRQOCPDNPETPM	362

```

RESULT      3
ID          Q95KC3
AC          Q95KC3;
DT          01-DEC-2001 (TREMBLrel. 19, created)
DT          01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT          01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE          HYPOTHEtical. 39.5 KDA PROTEIN.
OS          Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC          Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC          Cercopithecinae; Macaca.
OX          NCBI_TaxID=9541;
RN          [1]
RP          SPOURCE FROM N.A.
RC          TISSUE=MEADULLA OULOCALIA.
RA          Osada N., Hida M., Kusuda T., Tanuma F., Iseki K., Hirai M., Terao K.,
RA          Suzuki Y., Sugano S., Hashimoto K.;
RT          "Isolation of full-length cDNA clones from macaque brain cDNA
RT          libraries."
RL          Submitted (JUN-2001) to the EMBL/Genbank/DDBJ databases.
DR          EMBL; AB062981; HAH60747.1; --
DR          Hypothetical protein.
SQ          SEQUENCE 342 AA; 39479 MW; E93FC26BFFEEC4C CHe64;

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Query Match	Similarity	98.3%	Score 1748	DB 6	Length 342
Host/Local	Similarity	98.0%	Pred. No. 1,66	145	
Matches	335	Conservative	3	Mismatches	4
			Indels	0	Gaps
QY	1	MOAVNDLSAPGNTSLCTRDYKTCVPEPELVYLFVWLLTNGLAMRLEFPDIPKSNFI	60		
DB	1	MOALINDLSAPGNTSLCTRDYKTCVPEPELVYLFVWLLTNGLAMRLEFPDIPKSNFI	60		
QY	61	IFLKNTVTSIDLMILTFEPKILTSQAKLTGGELRTICQVTSVEFTWYISTSLGLTTI	120		
DB	61	IFLKNTVTSIDLMILTFEPKILTSQAKLTGGELRTICQVTSVEFTWYISTSLGLTTI	120		
QY	121	DHYQKTRPDKTSNDKNIIGAKIISVVIWAFWFLISLNNMLTFNKPRIKNNKCSFLKS	180		
DB	121	DHYQKTRPDKTSNDKNIIGAKIISVVIWAFWFLISLNNMLTFNKPRIKNNKCSFLKS	180		
QY	181	EEGLWVHELVNTICQVITWINEFLIVVYTLTKELYSRYVTROVGVKPPKVVAKVFI	240		
DB	181	EEGLWVHELVNTICQVITWINEFLIVVYTLTKELYSRYVTROVGVKPPKVVAKVFI	240		

OY	241	11AAVFICQVFFHARIPVTLLSOTRUVFDCVAHTLTFYKKESTIMLTSLNACLDPIITFF	300
Dh	241	11AVEFCVFEHFARIPTLSLRDFDCAEMTLFFYKESTIMLTSLNACLDPIITFF	300
OY	301	1CKSPRNLSISMICKPNSATSI SODNNKKRKDDCCDNNEFTPM	342
Dh	301	1CKSPRNLSISMICKPNSATSOSODNNKKRKDDCCDNNEFTPM	342
RESULT	4		
OC9CIV9	PRELIMINARY:	PRT:	347 AA.
DT	01-JUN-2001	(TREMBLrel_17, Last sequence update)	
DT	01-JUN-2001	(TREMBLrel_17, Last sequence update)	
DE	492150402381K PROTEIN (2900979622PK IP09YFIN)		
CN	P2RYI2 OR 4921504T24FK OR 2000979622BK		
OS	Mus musculus (Mouse)		
XC	Eukaryota; Eumetazoa; Chordata; Vertebrata; Euteleostomi;		
NCBI_TaxID=10990:	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;		
RN	SEQUENCE FROM N.A.		
RC	STEAIN-C57H/6J; TISSUP-TESTIS, AND HIPPOCAMPIUS;		
RC	MEDLINE-210B5660; PubMed-11217851;		
RA	Kawaji T., Shigaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,		
RA	Akawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,		
RA	Aizawa K., Iwasa M., Nishi K., Miyasawa H., Kondo S., Yamataka R.,		
RA	Sadato T., Okazaki Y., Gotohoriti T., Hono H., Kasukawa T., Saito R.,		
RA	Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,		
RA	Fleischmann W., Gaasterland T., Gliss C., King B., Koehnleush J.,		
RA	Kuehl P., Lewis S., Matsuo Y., Nakajin I., Pesole G., Quackenbush J.,		
RA	Schirml L.M., Stadl F., Suzuki R., Tomita M., Wagner L., Washio T.,		
RA	Hlake K., Okido T., Futano M., Anou H., Baldarelli P., Barsi G.,		
RA	Brockstein M.J., Butt C., Fletcher C., Fujita M., Gariboldi M.F.,		
RA	Gustinovich S., Hill D., Holman M., Hume D.A., Kamiya M., Lee N.H.,		
RA	Lyonis P., Marchionni L., Mashima J., MacFarrell J., Mompertis P.,		
RA	Nordone P., Ring B., Rimwald M., Rodriguez I., Sakamoto N.,		
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storck K.E.,		
RA	Suzuki K.I., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilting U.,		
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,		
RA	Hayashizaki Y.;		
RT	*Functional annotation of a full-length mouse cDNA collection.*		
RL	Nature 409:685-690(2001).		
DR	EMBL: AK014807; BAN29561.1;		
DR	EMBL: AK013804; BAN29000.1;		
DR	MGI: MGI:1918089; P21Y12.		
DR	MGI: MGI:1920308; Z930Z9B22PK		
DR	InterPro: IPR000276; GPCR_Rhodopsn		
DR	Pfam: PF00001; 7tm_1; 1.		
DR	PRINTS: PR00237; GPCRHHODOPS.		
DR	PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.		
SO	SEQUENCE: 347 AA; 39473 MW; F10748857E025F1 CRC64;		
Query Match	87.5%; Score 1555.5; DB 11; Length 347;		
Best local similarity	88.7%; Prod No 2.7e-131;		
Matches 299;	Conservative 16; Mismatches 21; Indels 1; Gaps 1		
OY	6	N1SAFGTSCCTFRVCCTGVLFELTYLVFFVLNTM:LAMPFPDPKSNFIIFLN	65
Dh	12	N1TFPGISTLCVRKYKTIOVLPFLTYLVFAALLINS:LAMRFQIRSKSNFIIFLN	71
OY	66	TWISOLLMITTPVKILSDAKLGGDLRFVCGVTSVFPYTWTLSISPLGLITIDBYOK	125
Dh	72	TWISLMLMIFFPKILSDAKLGAFLEFDVGCVTSVFETMTLSISFLGLITIDBYLK	131
OY	126	TTPPFSTPNKMLTVAKIISSVIAFMFNLSLPPNMILTNRDPDRKNVKKCSFLKSEFGLV	165
Dh	132	TTRPHKITSPPSNILGAKIISSVIAFMFNLSLPPNMILTNRDPDRKDKDVKCSFLKSEFGLV	191

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QY      186  WHELVNVCIOVEMINELIVVCTTLFKELYRSYVRGCVKPKRKAVWKKFIIIAVE    245
          |||||
Dh      192  WHELVNVCIOVEMINELIVVCTSLTKLELYRKYVTSGSAKKPKKVAKVFIIIAVF    251
          |||||
QY      246  FLCVPPEPPAPRIPTLTISOTRDVDFCAENLFLFYVKPSTMLWTLSINACLDHPVPHICRSP    305
          |||||
Db      252  FLCVPPEPPAPRIPTLTISOTRAVFDSCAENLFLFYVKPSTMLWTLSINACLDHPVPHICRSP    311
          |||||
QY      306  RNSLISMCLKPSNATSLSQDNKRKEKGSDPNNEEIPM    342
          |||||
Db      312  RNSLISMCLKSNS-ITISGTNNKKKOOOGESEETPM    347
          |||||

RESULT   5
QPREPX4 QPREPX4 PPELIMINARY: PRT: 343 AA.
ID QPREPX4;
AC QPREPX4;
DT 01-MAR-2001 (TREMblrel_16, Created)
DT 01-MAR-2001 (TREMblrel_16, Last sequence update)
DT 01-JUN-2001 (TREMblrel_17, Last annotation update)
DE FCY12 PLATELET ADP RECEPTOR.
OS Rattus norvegicus (Ral).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10110;
RX (1)
RN RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=21037966; PubMed=11196645;
RA Hollinger G., Jantzen H.-M., Vincent D., Li G., England L.,
RA Ramakrishnan V., Yang K.-H., Nurdin P., Nurdin A., Julius D.J.,
RA Conley P.B.;
RT Identification of the Platelet ADP Receptor Targeted by
KT Antithrombotic Drugs *
KL Nature 403:202-207(2001)
DR FMBI; AP313450; AAC64845.1;
DR InterPro; IPK00C276; GPCR_Pfamfsn
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00437; GPCR_HDOPSN.
DR PROSITE; PS50262; G_PROTEIN_RECIP_FL_2; 1.
KM Receptor
SU SDOUCECE 343 AA, 39047 MW, 7AFAPCPH56674136 CMC64;
```

Query Match	86.0%	Score 1528.5	DB 11	Length 344
Best local similarity	86.9%	Pred No. 6,9e-129		
Matches 293	Conservative 17	Mismatches 22	Indels 5	Gaps 1
QY	NLTSAQNTSLICRQYKLTQVLFPLLYVLPVGLITNGCLAMPLEPQIRKSNLTPLAKN	65		
DB	12 NITSLFGTSLCSKDKITQVLFELLYLVFLNGLITNSLAMPFFQIPKSNLTPLTOK	71		
QY	TVISDILMLITPPFKLTISDAKLGTCGRLKRTFCVGVITSVLFFETMVLSTISGLITTDWYOK	125		
DB	72 TVISDILMLITPPFKLTISDAKLGAGHRLFLYQGVITSVLFFETMVLSTISGLITTDWYOK	131		
QY	TTTPPKTSPNKNLTGAKTISVYIMLPMELLSLPMNLINBPQKKNVKKSEFLSEFLV	185		
DB	132 TTTPPKTSPSPNLGAKLTSLVALIWAAMPILSLIPMNLINRRKDKDITKCSPLASHPOLV	191		
QY	WHELVANTICGVTFW;NFI;VLYCYCTLTKEKELRYSVVPTRGCVKVRKKVNNKVPILIAVF	245		
DB	192 WHELVANTICGVTFW;NFI;VLYCYCTLTKEKELRYSVVPTRGSAKRPKRVNLIKVFILIAVF	251		
QY	FICVPPHFAKIPYTLISQTRDVFEDCAENLTLPYVKSLTLMITSLINAGLDPHLYFFELCKSF	305		
DB	252 FICVPPHFAKIPYTLISQTRAVFDCAENLTLPYVKSLTLMITSLINAGLDPHLYFFELCKSF	311		
QY	RNSLTSMKCKENSAFTSLQENRKKEDEGSDPNEETPM	342		
DB	312 RNSLTSMKCKENSAFTSLQENRKKEDEGSDPNEETPM	343		

[illegible]

QY 197 IFNFIPLIICVCIITLIRLEYSRYEIVROCVGPKKKVAWVFIIIAVEFIEPVPPEAR 256
 ||| : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
 DB 195 IEFVIFELIMLFVEYVIARKKYYDSYRKSCKDKKNKKKEGVFVVAVFTVCFAPIFEAR 254
 QY 257 IPYTISCTRIIVEPCATANIILFFVKFSHMIJSTNAFLDPVFTEFCNSFNSSLSMLKCP 316
 ||||| : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
 DB 255 VPHYSOTGNKKIKDRILONDIFIAKETETFLAAMINCMIDILYFLUCKKFKIKLMQW-IG 312
 QY 317 NSATSLSDNRKKKED 332
 || : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
 DB 313 KKTTASSDENHSSOTD 328

RESULT 7
 Q9DB12 PRELIMINARY: PRT: 337 AA.
 AC Q9DB12;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE 2010001L06PIK PROTEIN.
 GN GPP86 OR 2010001L06PIK.
 OS Mus musculus (Mouse).
 OC Eukaryota, Metazoa, Chordata, Clariata, Vertebrata, Euteleostomi,
 CC Mammalia, Eutheria, Rodentia, Sclerognathi, Muridae, Murinae, Mus.
 OX NCBI_TaxID=10090;
 RX [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57Bl/6J; TISSUE=SMALL INTESTINE;
 RK MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arkava T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izada M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Toyopori T., Tono H., Kasipawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Balow S.C., Casavant T.,
 RA Flitschmann W., Gaasterland T., Gissi C., King H., Kochwa H.,
 RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiraldi L.M., Stabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Sekido T., Furuno M., Arora H., Raddehalli P., Parish G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Butt C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hoffman M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombertis P.,
 RA Nordrup P., Ping B., Pinwald M., Rodriguez I., Sakamoto N.,
 RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,
 RA Suzuki H., Toyo-Oka K., Wada K.H., Welzl C., Whitaker G., Wilming L.,
 RA Wyshewski-Aoris A., Yoshida K., Hasagawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AK008013; BAB25409.1; -;
 DR MGI: MG11921441; GFr86.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm.1.1.
 DR PRINTS: PR000237; GPCRHHODPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PESTIDE: PSS0262; G_PROTEIN_RECEP_F1_2.1.
 DP SEQUENCE 337 AA: 38693 MW: 201476DFB93D5EA CR:64;

Query Match 44.7%; Score 794; OH 11; Length 337;
 Best Local Similarity 45.9%; Pred. No. 3, 2e-65;
 Matches 151; Conservative 63; Mismatches 111; Indels 4; Gaps

QY 6 NLTSAAPC-NFSICTRDYKKTVOVLPELYTVLFEVALITNCIAAKRFPGQRKSNFIFL 64
 ||| : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
 DB 6 NTTCMGCFSESRCKPRIMKMTQLTFPLVLYTVFVLAGLITNTVALMVAVHLIPSNFIFVL 65
 QY 64 KNVTYSLLMILFFPKRLISDAKLGTGLPTTVCVYTSVFTFYFTSYISFLGITTDKR 124
 ||||| : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
 DB 66 KNITVALDIIMALMKPKRLISDSIALHWQRCGVCLSSVVFYETMYVGMIMLCILAFDRP 125

QY 124 QKTRPFTSNKLLGAKILSVIWMFLLSLPNNILTRDPKRNKCKSEKSEF 183
 DB 126 LKIMPEKTFVKKIAFAIVSISIMPELISLNNIL-NKPEPSSVKKCKASLSPUG 184
 QY 184 LVMHPIVNICOVIMWIMELIVCYTLITRELYNSVVRTRGVKVRKVNKVFIIIA 243
 DB 185 LMMHGVSHITCOLITMAVILMLLEFVATKRVKNSYKFRSKDS-PHRELEVFIVMA 243
 QY 244 VFFICVPHFARIPYTLISQTRVDICAFANILFYVKESSTIMILSLNACLDPPFYFFICK 303
 DB 244 VFFICVPHFARIPYTLISQTRVDICAFANILFYVKESSTIMILSLNACLDPPFYFFICK 303
 QY 304 SFENSLISMLKCPNSATSLSDNKEKEDP 332
 DB 304 KFTQKVCVWVKAKRTAGSEPHHSSQTD 332

RESULT 8
 Q9956 PRELIMINARY: PRT: 338 AA.
 ID Q9956: 01-MAR-2001 (TREMblrel, 16, Created)
 DT 01-MAR-2001 (TREMblrel, 17, Last sequence update)
 DT 01-JUN-2001 (TREMblrel, 17, Last annotation update)
 DE 7 TRANSMEMBRANE G-PROTEIN COUPLED RECEPTOR.
 DE Mus musculus (Mouse).
 DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 DE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 DE NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lee B.C., Stradden D.T.:
 RA 7 Transmembrane G protein coupled receptor from hematopoietic
 RA precursors.
 RT Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF177211; AAC09275.1;
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: PF00601; 7tm 1; 1.
 DR PRINTS: PR00247; GPCR_RHODOPSIN.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_P1_2; 1.
 DR Receptor: Transmembrane.
 KW SEQUENCE 338 AA; 38861 MW; 437650622688AE CR64;

Query Match 41.7%; Score 741.5; DB 11; Length 338;
 Best Local Similarity 44.1%; Pred. No. 166-58;
 Matches 146; Conservative 69; Mismatches 109; Indels 7; Gaps 3;

QY 4 VDNLTAPNTSLCTRDYKITOVLEPLLYLVFFVGLITNGLAMRIFOLRSKSNFIIFL 63
 DB 1 MNSSTIDPPNCPGNNVTLITKQITIVYGVVFTCLLNGISCMIPFYVSSKSPITLYL 60
 QY 64 KNIVISDLMLTPEPKILSDAKIGTQPIRTFVQVTSVTFYFWYISISPLGLITIDRY 123
 DB 61 KNIVVAFMLTPEPKVLDNSIDIPWQVNVCEVSAVIEFVNNYVIVEFGDISPDY 120
 QY 124 QKTRPFTSNKLLGAKILSVIWMFLLSLPNNILTRDPKRNKCKSEKSEF 183
 DB 121 YKIVKPLITISVOSVANSKLSVIMVIMLILAVNIIITNGVKEVRIQCMELKNELG 180
 QY 184 LVMHPIVNICOVIMWIMELIVCYTLITRELYNSVVRTRGVKVRKVNKVFIIIA 243
 DB 181 KKHMKASNYIPVSPFWVVFLLIVFYALITRKIFKSHKSRKNSISVKKSSRNIPSVI 240
 QY 244 VFFICVPHFARIPYTLISQTRVDICAFANILFYVKESSTIMILSLNACLDPPFYFFICK 303
 DB 241 VFFICVPHFARIPYTLISQTRVDICAFANILFYVKESSTIMILSLNACLDPPFYFFICK 303
 QY 304 SPFR--NSLISM-LKCPNSATSLSDNKEKEDP 330
 DB 301 PFRKYLANKLIMSLKYN--DLFVSKTKRR 328

RESULT 9
 Q96J28 PRELIMINARY: PRT: 358 AA.
 ID Q96J28: 01-DEC-2001 (TREMblrel, 19, Created)
 DT 01-DEC-2001 (TREMblrel, 19, Last sequence update)
 DT 01-DEC-2001 (TREMblrel, 19, Last annotation update)
 DE CDNA FLJ14878 F13. CLONE FLAC1903248. WEAKLY SIMILAR TO PROBABLE
 DE G PROTEIN-COUPLED RECEPTOR.
 DE Homo sapiens (human).
 DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 DE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 DE NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE-PLACENTA;
 RA Isogai T., Oca T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
 RA Wagaizuma M., Hosofri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
 RA Watanabe S., Kimura K., Murakami K., Ishi S., Kawai Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuno Y.,
 RA Niromiya K., Iwayanagi Y.;
 RA "New human cDNA sequencing project."
 RT Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK027784; BAB5366.1;
 DR NCBI_TaxID=9606; 78227008930779 CR64;

Query Match 39.3%; Score 699.5; DB 4; Length 358;
 Best Local Similarity 42.6%; Pred. No. 96-55;
 Matches 140; Conservative 67; Mismatches 113; Indels 9; Gaps 5;

QY 6 NITSANG-NISLCTRYKITOVLEPLLYLVFFVGLITNGLAMRIFOLRSKSNFIIFL 64
 DB 25 NRSIDGKMLT---HNEEDTVLVLLIFVASILNGLAVMIFPHIRKRTSFIYLYK 81
 QY 65 NTVISDLMLTPEPKILSDAKIGTQPIRTFVQVTSVTFYFWYISISPLGLITIDRY 124
 DB 82 NIYVADLIMLTPEPKVLDNSIDIPWQVNVCEVSAVIEFVNNYVIVEFGDISPDY 120
 QY 125 QKTRPFTSNKLLGAKILSVIWMFLLSLPNNILTRDPKRNKCKSEKSEF 183
 DB 142 KVVAFEDSRMNYITFTKVLSCVWIMAVLSLPLITNGLTNGOPTEDNIDHCKSLSPVAV 201
 QY 185 VMEHPIVNICOVIMWIMELIVCYTLITRELYNSVVRTRGVKVRKVNKVFIIIA 243
 DB 202 KMHAVIYNSCLFVAVLVILICGYAISRYIKS-SQFISQSSRRPPIHNSIRVVA 259
 QY 244 VFFICVPHFARIPYTLISQTRVDICAFANILFYVKESSTIMILSLNACLDPPFYFFICK 303
 DB 260 VFFICVPHFARIPYTLISQTRVDICAFANILFYVKESSTIMILSLNACLDPPFYFFICK 303
 QY 304 SFENSLISMLKCPNSATSLSDNKEKEDP 330
 DB 320 SFSPLEFKSNIPFNSISLSVSRSE 348

RESULT 10
 Q9BY21 PRELIMINARY: PRT: 358 AA.
 ID Q9BY21: 01-JUN-2001 (TREMblrel, 17, Created)
 DT 01-JUN-2001 (TREMblrel, 17, Last sequence update)
 DT 01-DEC-2001 (TREMblrel, 19, Last annotation update)
 DE G PROTEIN-COUPLED RECEPTOR 87.
 DE GPR47 (GPR35).
 DE Homo sapiens (human).
 DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 DE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 DE NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE 21172992; PubMed 11274702;
 RA With reference to Schaller H.C., Hollebrand S.:
 RT "An expressed sequence tag (EST) data mining strategy succeeding in
 RC the discovery of new G protein coupled receptors."
 RD J. Mol. Biol. 307:799-813(2001).
 RE [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE 21458557; PubMed 1154155;
 RA Lee D.K., Nguyen T., Lyong K.P., Chong P., Vasil W.B., Arkhilo G.,
 RT Lewis T., Evans J.F., George S.R., O'Dowd B.F.:
 RT "Discovery and mapping of ten novel G-protein coupled receptor
 RT genes." (Gene 275: 84-91(2001)).
 RC 1. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC 1. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: AF2437763; AK01858.1;
 DR EMBL: AF411114; M126485.1;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm.1.1;
 DR PRINTS: PR00237; GPCRHDOPSN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1;
 DR PROSITE: PS00262; G-PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
 SQ SHOUNCE 359 AA; 41465 MW; PDB157295AB5010P CR64.

 Query Match 49.1%; Score 694.5; DB 4; Length 358;
 Best Local Similarity 42.2%; Pred. No. 276-54;
 Matches 169; Conservative 68; Mismatch 114; Indels 9; Gaps 5;

 QY 6 NLSANV NISCTROYKIIQVILFPLIVLVFVGLITNGIAMRIPEQIRKSNPTIEIK 64
 DB 1
 DB 25 NRSNGKRNKNTL INEPTIVLPAVLILFVASILNGIAVWIFPHLRKTSIEFLK 81
 QY 65 NIVSLMLITFEFKIISAKIGTSPLETVQVTSVFETPKYSTSEIGITIDQYQ 124
 DB 1
 DB 82 NIVADLMITFEFKIVHAGGQWYFKILKRTSVLFVANNSTIVHGLISIDRYL 141
 QY 125 KILPPTNLSPKKICANIIIVVIAWMLSLNNMLINQPKPKKKKSEIKSERGL 184
 DB 1
 DB 142 KVAAPKDSKMSYSLIFKLVSVVWVIAVLSLNLINLNGPTLELDHRSKLSPLGV 201
 QY 185 VMHIVNYIQVILFWINPLIVQVYILIKRLYSVVRIGCGKVPK KVVAVKPF111A 243
 DB 1
 DB 402 KMLIVTVYNS LEVAVLVLLISYIAISPYIKS -SPQTSQSSPKRINQSTIPVVA 259
 QY 244 VETITVPHFARFYTISQIRVFDTAENTLFYKESITMLTSLNACTDPIYFELCK 303
 DB 1
 DB 260 VPECELPYHDKIPFESHDLDELDESQKILYCKEETFLPACNVCIDPIYFEMCK 319
 QY 404 SPTNSI -SMKCPNSATSLQDNKKF 440
 DB 1
 DB 420 STSPETKRSNIPSPSTPESQVSPSE 448

 RESULT 11
 Q99MT7 PRELIMINARY PRT: 359 AA.
 AC Q99MT7;
 DT 01-JUN-2001 (TRENDEL 17, Created)
 DT 01-JUN-2001 (TRENDEL 17, Last sequence update)
 DT 01-DEC-2001 (TRENDEL 19, Last annotation update)
 DE G-PROTEIN COUPLED RECEPTOR GPR87.
 GN GPR87
 OS Mus musculus (Mouse).
 RA Fukaya et al. Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 RA Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RX NCBI Taxid 10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RD MEDLINE 21172992; PubMed 11274702;
 RA With reference to Schaller H.C., Hollebrand S.:
 RT "An expressed sequence tag (EST) data mining strategy succeeding in

RT the discovery of new G protein coupled receptors."
 RL J. Mol. Biol. 307:799-813(2001).
 CC 1. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC 1. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: AF295364; AK01866.1;
 DR MGI: 1944133; GPR87.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm.1.1;
 DR PRINTS: PR00237; GPCRHDOPSN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1;
 DR PROSITE: PS00262; G-PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
 SQ SHOUNCE 359 AA; 41462 MW; PDB130274PCDA CR64;

 Query Match 48.6%; Score 685.5; DB 11; Length 359;
 Best Local Similarity 41.7%; Pred. No. 176-53;
 Matches 146; Conservative 65; Mismatch 120; Indels 5; Gaps 4;

QY 8 TSAQNTSLCTROYKIIQVILFPLIVLVFVGLITNGIAMRIPEQIRKSNPTIEIK 67
 DB 1
 DB 26 STEGGKRNKNTLIRKIDTILFPLIVLVFVGLITNGIAVWIFPHLRKTSIEFLK 85
 QY 68 ISDLMLITFEFKIISAKIGTSPLETVQVTSVFETPKYSTSEIGITIDQYQ 127
 DB 1
 DB 86 VADLMITFEFKIVHAGGQWYFKILKRTSVLFVANNSTIVHGLISIDRYL 145
 QY 128 PEPFSPKRLTAKLISVIAVNFELSLPMMITNPEPRKRNKTSIEFLK 187
 DB 1
 DB 146 KPDQDSKMSYSLIFKLVSVVWVIAVLSLNLINLNGPTLELDHRSKLSPLGV 205
 QY 188 FIVNYIQVILFWINPLIVQVYILIKRLYSVVRIGCGKVPK KVVAVKPF111A 246
 DB 1
 DB 206 MAVTVDSCTFVAVLVILGCTYIAISPYIKS -SPQTSQSSPKRINQSTIPVVA 263
 QY 247 ICFVPHFARFYTISQIRVFDTAENTLFYKESITMLTSLNACTDPIYFELCK 306
 DB 1
 DB 264 TCELPYHDKIPFESHDLDELDESQKILYCKEETFLPACNVCIDPIYFEMCK 319
 QY 307 NSLI -SMKCPNSATSLQDNKK 340
 DB 1
 DB 324 RILPKKSNIRKESIRISQSVRSK 349

 RESULT 12
 Q9BE53 PRELIMINARY PRT: 228 AA.
 AC Q9BE53;
 DT 01-JUN-2001 (TRENDEL 17, Created)
 DT 01-JUN-2001 (TRENDEL 17, Last sequence update)
 DT 01-DEC-2001 (TRENDEL 19, Last annotation update)
 DE HYPOPHYSAL PROTEIN.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 RA Fukaya et al. Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 RX NCBI Taxid=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=FRONTAL CORTEX;
 RA Osada N., Hida M., Kusuda J., Tanuma K., Isoki K., Hirai M., Ito K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RT "Isolation of full-length cDNA clones from macaque brain cDNA
 RT libraries."
 RL Submitted (MAR 2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB056816; BAB39342.1;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm.1.1;
 DR PRINTS: PR00237; GPCRHDOPSN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; UNKNOWN_1;
 DR PROSITE: PS00262; G-PROTEIN_RECEP_FL_2; 1.
 SQ SHOUNCE 228 AA; 26156 MW; 479075DMHMD22C CR64;

GenCore version 4.5
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OM protein - protein search, using SW model

Run on: August 21, 2002, 15:44:28 Search time: 13.43 Seconds
(without alignments) 986 008 Million cell updates/sec

Title: US-09-780-576-2

Perfect score: 1778

Sequence: 1 MOAVDPNLTSAQNTSLCTRP

ALIGNMENTS

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing list: 45 summaries

Database: SWISSPROT_40*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	772	43.4	349	1 K101_HUMAN	Q15391 homo sapien
2	694	39.0	305	1 K101_HUMAN	Q35881 ratius norv
3	488	27.4	319	1 H963_HUMAN	Q14626 homo sapien
4	411.5	21.1	376	1 C9RY_MOUSE	Q97186 mus musculu
5	409.5	21.0	381	1 GPRY_HUMAN	Q90656 homo sapien
6	394	21.2	342	1 PAFR_HUMAN	P21556 camo porce
7	392.5	21.1	342	1 PAFR_HUMAN	P12249 homo sapien
8	379.5	21.3	361	1 BH12_HUMAN	Q95603 sus scrofa
9	367	20.6	345	1 CLT2_PIG	Q62035 mus musculu
10	366	20.6	341	1 PAFR_MOUSE	P46002 ratius norv
11	362	20.4	342	1 PAFR_PAT	P32250 gallus gall
12	357.5	20.1	346	1 P2Y6_HUMAN	Q98875 homo sapien
13	347.5	19.5	346	1 CLT2_HUMAN	P79928 xenopus lae
14	347.5	19.5	537	1 P2Y8_XENLA	Q92061 mus musculu
15	344	19.3	309	1 C172_MOUSE	Q92459 ratius norv
16	339.5	19.1	309	1 C172_PAT	P25104 bos laurus
17	339	19.1	359	1 AG2R_BOVIN	Q77550 ovus aries
18	338	19.0	344	1 P2Y5_HUMAN	Q13304 homo sapien
19	334	18.8	359	1 AG2R_SHEEP	Q13725 homo sapien
20	329.5	18.5	349	1 GPRH_HUMAN	Q13725 homo sapien
21	329	18.5	359	1 AG2S_HUMAN	Q13725 homo sapien
22	328	18.4	340	1 CLT1_PIG	Q95603 sus scrofa
23	327	18.4	359	1 AG2P_PIG	P30555 sus scrofa
24	325	18.3	359	1 AG2P_CANFA	P43240 canis fami
25	323.5	18.3	359	1 PAR2_MOUSE	P55086 mus musculu
26	321	18.3	359	1 AG2R_KAHIT	P14976 otyctoagrus
27	321	18.1	359	1 AG2R_HUMAN	P30556 homo sapien
28	320	18.0	359	1 AG2P_HUMAN	Q94677 homo porce
29	320	18.0	370	1 P2Y9_HUMAN	Q15743 homo sapien
30	319.5	18.0	365	1 GPR6_HUMAN	P25095 ratius norv
31	319	17.9	359	1 AG2R_PAT	P24089 ratius norv
32	319	17.9	359	1 AG2S_PAT	P24089 ratius norv
33	318	17.9	359	1 AG2R_MOUSE	P24089 mus musculu

34	316.5	17.8	398	1 OPRM_RAT	P13355 ratius norv
35	316	17.8	359	1 AG2S_MOUSE	P29755 mus musculu
36	316	17.8	377	1 AP1_RAT	Q97186 ratius norv
37	316	17.8	397	1 PAR2_RAT	Q63645 ratius norv
38	313.5	17.6	380	1 AP1_HUMAN	P35414 homo sapien
39	313.5	17.6	401	1 OPRM_PIG	Q95247 sus scrofa
40	312	17.5	359	1 AG2R_HUMAN	Q35210 meriones un
41	312	17.5	401	1 OPRM_BOVIN	P79350 bos laurus
42	311	17.5	369	1 PAR3_MOUSE	Q08675 mus musculu
43	310.5	17.5	362	1 AG2R_XENLA	P32303 xenopus lae
44	310.5	17.5	363	1 AG2S_XENLA	P32303 xenopus lae
45	310	17.4	374	1 PAR3_HUMAN	Q00254 homo sapien

RESULT 1
K101_HUMAN STANDARD; PRT; 338 AA.
ID K101_HUMAN
AC Q15391;
DT 15-JUL-1998 (Ref. 36, Created)
DT 15-JUL-1998 (Ref. 36, Last sequence update)
DT 30-MAY-2000 (Ref. 39, Last annotation update)
DE Probable G protein-coupled receptor KIAA0001.
GN KIAA0001.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID:9606;
IL 111
RN SEQUENCE FROM N.A.
RP TISSUE-BONE marrow;
RC MEDLINE-96051387; PubMed-7584026;
RA Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawabayashi Y.,
Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;
RA "Prediction of the coding sequences of unidentified human genes. I.
The coding sequences of 40 new genes (KIAA0001-KIAA0040) derived by
analysis of randomly sampled cDNA clones from human immature myeloid
cell line KG-1."
RL DNA Ref. 1:27-35(1994)
RL FUNCTION: OPRM1 RECEPTOR
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC PROBABLE ORTHOLOG OF RAT VTR 15-20.
CC
CC This SWISS-Prot entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
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entities requires a license agreement (see <http://www.isb-sib.ch>).
CC or send an email to license@sib.ch.
CC
CC EMBL: D13626; BAA02791.1; -
CC CCRDB: GCR-0594;
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; FALSE NEG.
DR PROSITE: PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor, 7 transmembrane, glycoprotein,
PT DOMAIN 1 29
FT TRANSMEM 30 55
FT DOMAIN 51 55
FT TRANSMEM 56 76
FT DOMAIN 77 96
FT TRANSMEM 97 117
FT DOMAIN 118 139
FT TRANSMEM 140 160
FT DOMAIN 161 188
FT TRANSMEM 189 209
FT DOMAIN 210 234
FT TRANSMEM 235 255

DR	Pfam: PF00001; 7tm_1; 1.
DR	PRINTS: PR00237; GTPROTEIN_RECEP_FL_1;
DR	PROSITE: PS00237; G_PROTEIN_RECEP_FL_1;
DR	PROSITE: PS00262; G_PROTEIN_RECEP_FL_2; 1.
KW	Receptor; G-protein coupled receptor; Transmembrane; glycoprotein.
FT	DOMAIN 1 61
FT	TRANSMEM 62 82
FT	DOMAIN 83 88
FT	TRANSMEM 89 109
FT	DOMAIN 110 128
FT	TRANSMEM 129 149
FT	DOMAIN 150 171
FT	TRANSMEM 172 192
FT	DOMAIN 193 216
FT	TRANSMEM 217 237
FT	DOMAIN 238 259
FT	TRANSMEM 270 290
FT	DOMAIN 291 310
FT	TRANSMEM 311 331
FT	DOMAIN 332 381
FT	DISULFID 127 204
FT	CARBOHYD 28 28
FT	CARBOHYD 36 36
FT	CARBOHYD 42 42
FT	CANONIC 200 200
FT	CARBOHYD 295 295
FT	CONFLICT 181 181
SQ	SEQUENCE 381 AA; 43860 MM; 491FC0165624579 CRC64;

Query Match	23.0%	Score 409.5;	DI 1;	Length 381;
Host local Similarity	32.3%;	Pred. No. 6,7e 21;		
Matches 102;	Conservative 53;	Mismatches 152;	Indels 9;	Gaps 7;

DQ	2 QAVDNLSAGNSLSTLRDYKITVLFLLTTLVFLEFVLITLNGLAMIFQHSKSNFI-60
DB	32 QPPONSATP-NWTTCPPMDCKLISLVLTTSVIPVGLGNLIYVPLGIRKRNSTO-90
QY	61 IFLKNVISDLMLLPFKRILSDAKLTGDFRFVCVTSVIEFYMTYSISFLIITI-120
DB	91 IYLLNVAIDLILLFCLPRIMYHINOKMKTLGVILRKVGCTLEYMNYISILLFLISL-150
QY	121 DRQKTRIPPKYSNRKNLGAKILSLVIAWAPHLAIIPLNNMLINKOPRDKNVKKCSFLKS-180
DB	151 DRYIKINRSIQQRALITTKOSIVGCCIW-MLAISGEFLMIILLKKGKINSTCFEHD-209
QY	181 EFGIWHIEINYNGVAFINFLIVCYTTLITRELY-SVVRFR-GVGRVPRKVXVK-237
DB	210 KHNAKGAHPNPIIVMPHLPLILLISYIKICKNILMSKRSKPIINSKYAIIARKN-267
QY	238 VETIAVFEICVEPFHFARIPYLISQIKGVDCGTAEINTLEVYEKESTIMLTSLNACIDPTI-297
DB	268 SFVILLIFTCEVPYHAFFRIYISSQLNVSSGYKEIVERTINEIMLVLSFSFSCIDPVW-326
QY	298 YFLICKSPNLSISM-313
DB	327 YFLMSSNIIRIKIGQL-342

RESULT	6		
PAPR_HUMAN	STANDARD;	PRT:	342 AA.
AC	P25105;		
CT	01-MAY-1992 (Rel. 22, created)		
DT	01-MAY-1992 (Rel. 22, last sequence update)		
ST	16-OCT-2001 (Rel. 40, last annotation update)		
DE	Platelet activating factor receptor (PAF-R).		
CN	PAFR OR PAFR		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
NC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;		
OX	NCBI_TaxID=9606;		
NN	[1]		

QY 400 EVKSPRN SLISMKCPNSAT 420
 11 11 11 11 11 11
 DB 295 ELKKERKLEKREY-SFSPAT 422

RESULT

11 PAFR_VAVR0 STANDARD: PRI: 342 AA.

AC P21566

01 MAY 1991 (rel. 18, created)

01 OCT 1991 (rel. 19, last sequence update)

01 OCT 1996 (rel. 44, last annotation update)

01 OCT 1996 (rel. 44, last annotation update)

01 OCT 1996 (rel. 44, last annotation update)

01 OCT 1996 (rel. 44, last annotation update)

01 OCT 1996 (rel. 44, last annotation update)

01 OCT 1996 (rel. 44, last annotation update)

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01 OCT 1996 (rel. 44, last annotation update)

Query Match 22.1% Score 392.5, DB 1, Length 442;
 Best Local Similarity: 30.7%, Pred No. 8, 3e 20;
 Matches 103; Conservative 66; Mismatches 140; Indels 21; Gaps 9;

QY 20 DYKIVVAPLAVTVLVPVQVLTNGLAMRPFQI--RSKSNPT-PLKNTVSDMLMT 76

DB 10 DSEFRTLPFVYSIIIFVIGLIVANCYVLMVFAHFKSKLNEIKIFMNLIVADLLFLIT 69

QY 77 PFKRLSDAKLGTGPKLVQVIVSIFEFMTYISISFLGLITDKYKTRFKTSNPK 136

DB 70 LPLMIVYSNQGMPFPRKFCINLACLPFINTGVSAPLVITNKKVQAVVPIKIAQAT 129

QY 137 NLGAKLISVAVI--AFMFLISDPMILINRQIRKKNVKSQSPKSEFG--LVWH 187

DB 130 TRRGIALSLVTVVAVVAAVSFLVNDISNNVSNNGSNITRC-FEIKYKSKVLLII 188

QY 188 EIVNVCQV-IVNPLIVCYTLITKLYSVYFRQGVKPKKVVAVFIIIAVVF 246

DB 189 -ICIVIGPFIIVPLIIFCMVLIHTLIRQPKQONAVF-RRALMVQIVIAVVF 242

QY 247 ICFVPHFARIPYTESGTCVETCTANTLEVKESIIISLNLCTEPIYFELFKSR 406

DB 243 ICVPHFMVQIVITLAIL-GMIPSSNHOAINAHQVITCLISTNCVLDVIVCFILKFR 401

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DB 302 KILSEKINIRSSQKCSRVITDTGFMALPINRTV 337

QY 307 NSLISMLKCPNSAVSLSDNRRKKFQDQGNPRTM 342

DR PROSITE: PS00237, G-PROTEIN_RECEP_F1_1, 1.
 DR PROSITE: PS00262, G-PROTEIN_RECEP_F1_2, 1.
 KM G-protein coupled receptor, transmembrane, glycoprotein.
 FT DOMAIN 1 31
 FT TRANSMEM 32 57
 FT DOMAIN 58 77
 FT TRANSMEM 78 95
 FT DOMAIN 96 105
 FT TRANSMEM 106 127
 FT DOMAIN 128 149
 FT TRANSMEM 150 168
 FT DOMAIN 169 192
 FT TRANSMEM 193 215
 FT DOMAIN 216 241
 FT TRANSMEM 242 265
 FT DOMAIN 266 287
 FT TRANSMEM 288 312
 FT DOMAIN 313 361
 FT DOMAIN 126 144
 FT DISOIID 104 181
 SO SEQUENCE 361 AA: 41224 MW: 55A2171F4C9C9B7B CMC9A;

Query Match 21.3% Score 379.5; DB 1; Length 361;
 Best Local Similarity 26.0%; Pred. No. 6,5e-19;
 Matches 94; Conservative 84; Mismatches 152; Indels 31; Gaps 11;

OY 1 MOAVDNI.F---SAPDNTSLCTRDYKLTQVLPPLATYVLPFGCLITNGIAMRIFPOIRSK 56
 DB 3 IQMANNFTSPASPTPOGNDCLVIAHISTARIYMLPLHSVLEIIGVGNLALAVYQNRKK 62
 OY 57 SN.FIFLKNVYISDLMLITPEPKL-----SDAKLGTPRTYCOVTSVFYTMKI 110
 DB 63 INSTLYSTNLVLSDFLPTALPRTIAYVAMGPDWRIQGA-----LCRTALAVFYINITY 117
 OY 111 STIFLLITIDPYUKTTPREKTSNEKNLAKRTLSVIVAMFLLSEPMI--LTNHPQR 168
 DB 118 GVMFMCISLDKFLAVVHLERIKRIEHAQVCLFVWLVEAQLPLILNMSQDVE 177
 OY 169 DKNVKKCSFKISFEGLVWHPVYVYICQVLPWIFLVIVCYTLITKELYS-----YVVF 223
 DB 178 FITCMETPNEETKSLPM--ILGACFICVPLPLITLIFYSQVYKLPRTAKUNPLEK 245
 OY 224 PCVKKPRKRVKVVITTAVFVTVVPHFAPITVLSGTR--GVFDTAENTLIFYVE 281
 DB 236 GGVNKK---KALNI--LIIIVVLCFPPYVALIOMIKKLRKSNLFCOSQKHSFJLSH 291
 OY 282 STIMLTSLNGLDPEIFETFLCKSEKSLISMLKTFNSATLSQFNKKRKLCTEPEEIP 341
 DB 292 FTYCLNENCMPLIYFFACRKYKRYKVMNKL-POVSVSISAVKAPDEENREMTETQ 350
 OY 342 M 342
 DB 351 M 351

RESULT 9
 CLUSTAL_PIG STANDARD PPT: 345 AA.
 AC Q95N03;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DK Cysteine leucokine receptor 2 (CysLtr2).
 GN CysLtr2 OR CysLtr2.
 OS Sus scrofa (Pig).
 OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
 OC Mammalia, Eutheria, Cetartiodactyla, Suinae, Suidae, Sus
 OX NCBI_TaxID=9823;
 RN 111
 RP SOURCE FROM N.A.
 RA Kamohara M., Takasaki T., Matsumoto M., Matsumoto S., Saito T.,
 Ohishi T., Soga T., Matsushima H., Furutachi K.;

*Characterization of the cloned rat and porcine cysteinyl leukotriene
 receptors.*
 RL Submitted (DUC-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for cysteinyl leukotrienes. The response is
 mediated via a G-protein that activates a phosphatidylinositol
 calcium second messenger system (by similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL, co-station -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb.ch/announce/>
 or send an email to license@isb.sib.ch).

DR EMBL: AB052662; BAB08417 1;
 DR InterPro: IPR000276; GPCR_Phdpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE: PS00237, G-PROTEIN_RECEP_F1_1, FALSE NEG.
 DR PROSITE: PS00262, G-PROTEIN_RECEP_F1_2, 1.
 KM G-protein coupled receptor, transmembrane, glycoprotein.
 FT DOMAIN 1 43
 FT TRANSMEM 44 64
 FT DOMAIN 65 73
 FT TRANSMEM 74 94
 FT DOMAIN 95 124
 FT TRANSMEM 125 145
 FT DOMAIN 146 154
 FT TRANSMEM 155 175
 FT DOMAIN 176 205
 FT TRANSMEM 206 226
 FT DOMAIN 227 246
 FT TRANSMEM 247 267
 FT DOMAIN 268 287
 FT TRANSMEM 288 308
 FT DOMAIN 309 345
 FT DISOIID 112 188
 FT DISOIID 20 20
 FT CARBOHYD 29 29
 FT CARBOHYD 177 177
 FT CARBOHYD 184 184
 SO SEQUENCE 345 AA: 39410 MW: 51B1F846465655 CPC64;

Query Match 20.6% Score 367; DB 1; Length 345;
 Best Local Similarity 29.0%; Pred. No. 4.3e-18;
 Matches 93; Conservative 72; Mismatches 134; Indels 22; Gaps 9;

OY 1 MOAVDNLISAPGNTSLCTRDYKLTQVLPPLATYVLPFGCLITNGIAMRIFPOIRSKSNFI 60
 DB 17 MEPNSTLGNHNSRSCTEENK--REHYVIVYVLPWCAI/GNGHSIVYLPKRYKRSYV 74
 OY 61 -FEKNTVYISDLMLITPEPKI-----LSDAKLGTPRTYCOVTSVFYTMYSIF 114
 DB 75 NVFMNLAIISDLITPLTPREKDYLLKSNKIHGIDP-----CRIMSVSMVNNYSIYF 129
 OY 115 IGLITIDPYUKTTPREKTSNEKNLAKRTLSVIVAMFLLSEPMI--LTNHPQR 168
 DB 130 LIVLSVPRFLATVHPPEFLHTTSIKNMTIGGVIV--IFIMNSSTVLLKNSSEQDNTVL 187
 OY 175 GSFKSPQCVLWHPVYVYICQVLPWIFLVIVCYTLITKELYSYVPCVCKVPEEF 233
 DB 188 CLELNSN-KVTKLKTMMNVVALVGVLPFGTSLCYLIIHALIKVIVPSGL-RLSHRK 245
 OY 244 VAVKVEFIIIAVPEFVIFHFAIFEYVLSLTPVTV--TAENTLIFYVEFTSLTSTANT 293
 DB 246 ALITVIALIIFLQCFELPHVHLRIHLEWKAD-----CKKDRIKRAVAVATIALAANSQF 301
 OY 294 DPEIYFPLCKSPRNSLISMLK 314
 DB 302 NEFLYFACENFKRDKLSALR 322

RESULT 10

PAIR MOUSE STANDARD: PRT: 341 AA.

15-000-1998 (Rel. 36, Created)

15-000-1998 (Rel. 36, Last sequence update)

15-000-1998 (Rel. 36, Last annotation update)

15-000-1998 (Rel. 36, Last annotation update)

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15-000-1998 (Rel. 36, Last annotation update)

15-000-1998 (Rel. 36, Last annotation update)

Best Local Similarity 29.9%; Pred. No. 4,9e-18;
Matches 96; Conservative 64; Mismatches 133; Indels 28; Gaps 10;

20 DKTQVLPFLVLEFVGLITNGLAMRIFED--RSKSNFI-TLTKNTVLSLLMILT 76

10 DSEPRYTLFPIVSVIFHGVANGVYIWFANLYPSKLINEIKIKVMNLMADLFLI 69

77 PPFETLSAKNGCPHTEFCOVSVIFPEIWMISIFGLIITIDYOKTIRPKISNR 136

70 LPLMIVYYNEDGWLIFNPLCNAGCLEFFINTCSVAFELVITNROAVYIKTKAQ 129

137 NLGAKLLSVYIAPM-----PILSLPNNMLINRQPRKVKKSPKSPKSG-- 188

130 TRKGISLISLWISIVATASPLATDSNIYPNKDSNMLRCPHRYPSVPIVAV 189

189 IVNYICQVIMINFLI-VIACYLLIKELRSVRTGVSQVKKVKNVAVFIIVFPI 247

190 FIACPFLVPLIIFYCNVILHILITDPMKQ--KAGV-----KRAIMWCTVIAV 243

248 CVPFPRFARIPYTLISQTRDVEDCTAENTLIFYKSHILMLISLNACADUPEYFPIKSPFN 307

244 CVPFHVYVGLPMTLAEIG--YGFNFQAINDAIGITLITLSTNVLDPVLYITLKKER 301

308 -----SLISMLKCPNSATS 321

302 HLSKPYMSRMSRKC-SKATS 321

RESULT 11

PAIR: RAT STANDARD: PRT: 341 AA.

15-000-1995 (Rel. 32, Created)

15-000-1995 (Rel. 32, Last sequence update)

15-000-1995 (Rel. 32, Last sequence update)

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15-000-1995 (Rel. 32, Last sequence update)

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia, Pipoidae; Pipidae;
 CC Xenopodidae; Xenopus.
 CC NCBI_TaxID=8335;
 RN 111
 RP SEQUENCE FROM N.A.
 RC TISSUE-Neural plate;
 RX MEDLINE:97284734; PubMed:9139711;
 RA Jordanov V D., Dale I., King H.F., Whitlock N., Hornstock G.;
 RT "Early expression of a novel nucleotide receptor in the neural plate
 of Xenopus embryos";
 PL J. Biol. Chem. 272:12583-12590(1997).
 CC -1- FUNCTION: RECEPTOR FOR EXTRACELLULAR ATP, GTP, CTP AND UTP.
 CC THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
 CC ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
 CC MAY PLAY A KEY ROLE IN THE EARLY DEVELOPMENT OF NEURAL TISSUE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC This SWISS-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC EMBL: X99563; CAA68213.1;
 DR HSSP: P34966; IDDD.
 DR GCRDB: GCR_1419;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; G-PROTEIN RECP_F1_1; 1.
 DR PROSITE: PS00237; G-PROTEIN RECP_F1_2; 1.
 DR PROSITE: PS00262; G-PROTEIN RECP_F1_2; 1.
 KM G-protein coupled receptor: Transmembrane; Glycoprotein
 FT DOMAIN 1 49 EXTRACELLULAR (POTENTIAL)
 FT TRANSMEM 50 70 1 (POTENTIAL)
 FT DOMAIN 71 79 CYTOSOLASMIC (POTENTIAL)
 FT TRANSMEM 80 100 2 (POTENTIAL)
 FT DOMAIN 101 118 EXTRACELLULAR (POTENTIAL)
 FT TRANSMEM 119 139 3 (POTENTIAL)
 FT DOMAIN 140 161 CYTOSOLASMIC (POTENTIAL)
 FT TRANSMEM 162 182 4 (POTENTIAL)
 FT DOMAIN 183 210 5 (POTENTIAL)
 FT TRANSMEM 211 231 CYTOSOLASMIC (POTENTIAL)
 FT TRANSMEM 232 254 6 (POTENTIAL)
 FT TRANSMEM 255 275 7 (POTENTIAL)
 FT TRANSMEM 276 292 8 (POTENTIAL)
 FT TRANSMEM 293 316 9 (POTENTIAL)
 FT DOMAIN 317 337 CYTOSOLASMIC (POTENTIAL)
 FT DOMAIN 338 357 CYTOSOLASMIC (POTENTIAL)
 FT DOMAIN 358 377 CYTOSOLASMIC (POTENTIAL)
 FT CARBOHYD 116 193 N-LINKED (GLCNAC...) (POTENTIAL)
 FT CARBOHYD 26 26 N-LINKED (GLCNAC...) (POTENTIAL)
 FT CARBOHYD 29 29 N-LINKED (GLCNAC...) (POTENTIAL)
 SEQUENCE 537 AA: 62024 MW: 10274612 Da; pI=4.2; pKa=6.4.

CC Query Match 19.58; Score 347.5; DR 1; Length 537;
 CC Best local Similarity 29.38; Prod No 1 3e-16;
 CC Matches 943; Conservative 60; Mismatches 157; Indels 7; Gaps 5.
 CC 1 MOAVIDLTARPNSTCTGDKYITQVLPFLTYVLFVGLITNGLAMRFF-QISKSNF 59
 DB 21 MKLMLMLN-DTEHDCVDFHCKPLIPVSAVPMVGLPINAMVFLAKMRWNPT 78
 CC 60 IIFLKTVSDLMITFEFKILSDAKLTGPIRTFVCVTSVFIFETVYISSEGLT 119
 DB 79 TYMFMFLSDILYVSLFTLYYYVDKNNMPGEVLCGLVFLFYANIKSSILELTG 138
 CC 120 IDRYOKTTPFKISNPKNLGAKILSVLIWAFMPLSLSPNMILTNQPKDKVKKCSPIK 179
 DB 139 VHPYGVCHPITSLPNNAKILVYVIALVWLVSITLTVPNLFEVTVSPVKNTIHDTP 198
 CC 180 SEPLWHEITVNYICGVLEWIMNFIIVCYTLITKELESVPTGVSXVPRKRVNK 247
 DB 199 PDPRARYVSTALMCLGIPCLIIACCYGLMRELMKPIVSGNOOLISYKRSIKTI 258
 CC 238 VPIIAVPCVPPHARIPYTLISQTRVDYDCAENILYVKKESILMLISNACLPPI 297
 DB 299 IFVMAI-FAIFPMPEHITPTIYYAPILGI-KYALVNIYTVVTPPLSANSCTPIL 316
 CC 298 YFPIICKSPRNSLSIMK 314
 DB 317 YELANDRYRRIIRVR 333
 CC RESULT 15
 CC ID CIFT2_MOUSE STANDARD; PRT; 309 AA.
 AC 0920AT;
 DT 01-MAR-2002 (Ref. 41, Created)
 DT 01-MAR-2002 (Ref. 41, Last sequence update)
 DT 01-MAR-2002 (Ref. 41, Last annotation update)
 DE Cystinyl leukotriene receptor 2 (CysLT2).
 GN CysLT2 OR CysLT2.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sclerogathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN 111
 RP SEQUENCE FROM N.A.
 RC TISSUE-Heart;
 RX PubMed:11591709;
 RA Bai Y., Yang G., Galycinski H., Figueroa D., Austin G.P.,
 RA Copeland N.G., Gilbert D.J., Jenkins N.A., Funk G.D.;
 RT "The murine cystinyl leukotriene 2 (CysLT2) receptor, cDNA and
 RT genomic cloning, alternative splicing, and in vitro
 RT characterization";
 FT J. Biol. Chem. 276:47480-47495(2001).
 CC -1- FUNCTION: Receptor for cystinyl leukotrienes. The response is
 CC mediated via a G-protein that activates a phosphatidylinositol
 CC calcium second messenger system. The rank order of affinities for
 CC the leukotrienes is LTC4 > LTD4 > LTE4.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Widely expressed at low levels, with highest
 CC expression in the spleen, thymus and adrenal gland, and lower in
 CC the kidney, brain and peripheral blood leukocytes.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC This SWISS-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC EMBL: AF31658; AK97354.1;
 DR InterPro: IPR000276; GPCR_Rhodopsn
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE: PS00237; G-PROTEIN RECP_F1_1; FALSE-NEG.
 DR PROSITE: PS00262; G-PROTEIN RECP_F1_2; 1.
 KM G-protein coupled receptor: Transmembrane; Glycoprotein
 FT DOMAIN 1 26 EXTRACELLULAR (POTENTIAL)
 FT TRANSMEM 27 47 1 (POTENTIAL)
 FT DOMAIN 48 56 CYTOSOLASMIC (POTENTIAL)
 FT TRANSMEM 57 77 2 (POTENTIAL)
 FT DOMAIN 78 98 3 (POTENTIAL)
 FT TRANSMEM 99 119 4 (POTENTIAL)
 FT DOMAIN 120 138 CYTOSOLASMIC (POTENTIAL)
 FT TRANSMEM 139 159 5 (POTENTIAL)
 FT DOMAIN 160 187 6 (POTENTIAL)
 FT TRANSMEM 188 208 7 (POTENTIAL)
 FT DOMAIN 209 229 8 (POTENTIAL)
 FT TRANSMEM 230 250 9 (POTENTIAL)
 FT DOMAIN 251 271 EXTRACELLULAR (POTENTIAL)

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OM protein - protein search, using sw model

Run on: August 21, 2002, 15:42:12 : Search time 13.1 Seconds

(without alignments)
637,676 Million cell updates/sec

Title: US-09-780-576-2

Perfect score: 1778

Sequence: 1 MOAVDNILTSAPCNISLCTRP SCNNPKKFGCGNPNFPPW 342

Scoring table: BLOSUM62

Gapop 10.0 : Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 98

Maximum Match 100%

Listing first 45 summaries

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1778	100.0	342	US-08-852-824-2	Sequence 2, Appli
2	823	46.3	333	US-09-221-456-2	Sequence 2, Appli
3	823	46.3	333	US-09-558-740-2	Sequence 2, Appli
4	797	44.8	333	US-08-812-871-1	Sequence 1, Appli
5	772	43.4	325	US-08-467-948A-29	Sequence 29, Appli
6	772	43.4	325	US-08-467-947A-29	Sequence 29, Appli
7	772	43.4	338	US-08-988-876-8	Sequence 8, Appli
8	772	43.4	338	US-09-303-524A-2	Sequence 2, Appli
9	679.5	38.2	358	US-08-988-876-9	Sequence 9, Appli
10	546.5	30.7	293	US-08-467-948A-6	Sequence 6, Appli
11	546.5	30.7	293	US-08-467-947A-6	Sequence 6, Appli
12	488	27.4	319	US-08-702-344-28	Sequence 28, Appli
13	410.5	23.1	326	US-08-118-270-39	Sequence 39, Appli
14	410.5	23.1	326	PCT-US93-08528-39	Sequence 39, Appli
15	392.5	22.1	342	US-08-988-876-9	Sequence 9, Appli
16	379.5	21.3	361	US-08-383-750-4	Sequence 4, Appli
17	379.5	21.3	361	US-08-452-678-4	Sequence 4, Appli
18	379.5	21.3	361	PCT-US93-09636-14	Sequence 4, Appli
19	376	21.2	348	US-08-852-824-17	Sequence 17, Appli
20	374.5	21.1	381	US-08-467-947A-30	Sequence 30, Appli
21	374.5	21.1	381	US-08-911-320A-2	Sequence 2, Appli
22	374.5	21.1	381	US-09-217-101-2	Sequence 2, Appli
23	349.5	19.7	302	US-08-467-948A-30	Sequence 30, Appli
24	349.5	19.7	302	US-08-467-947A-30	Sequence 30, Appli
25	349	19.1	344	US-08-467-948A-8	Sequence 8, Appli
26	339	19.1	344	US-08-467-947A-8	Sequence 8, Appli
27	337	19.0	468	US-08-907-221-127	Sequence 327, App

28	329.5	18.5	339	1	US-08-153-848-44	Sequence 44, Appli
29	329.5	18.5	339	2	US-08-812-871-3	Sequence 3, Appli
30	329.5	18.5	339	4	US-09-843A-44	Sequence 44, Appli
31	329.5	18.5	339	4	US-09-088-337B-44	Sequence 44, Appli
32	329.5	18.5	339	5	PCT-US93-11151-44	Sequence 44, Appli
33	329.5	18.5	339	5	PCT-US95-07180-2	Sequence 2, Appli
34	329	18.5	359	1	US-08-041-219A-6	Sequence 6, Appli
35	329	18.5	359	1	US-08-417-122-6	Sequence 6, Appli
36	327.5	18.4	395	1	US-08-097-938-2	Sequence 2, Appli
37	327.5	18.4	395	1	US-08-476-000-2	Sequence 2, Appli
38	327.5	18.4	395	1	US-08-472-840-2	Sequence 2, Appli
39	327.5	18.4	395	2	US-08-476-976-2	Sequence 2, Appli
40	327.5	18.4	395	3	US-08-474-410-2	Sequence 2, Appli
41	325.5	18.3	395	4	US-08-486-673B-2	Sequence 2, Appli
42	325.5	18.3	395	4	US-08-486-673B-5	Sequence 5, Appli
43	325.5	18.3	399	1	US-08-476-000-61	Sequence 61, Appli
44	325.5	18.3	399	1	US-08-472-840-61	Sequence 61, Appli
45	325.5	18.3	399	2	US-08-476-976-61	Sequence 61, Appli

ALIGNMENTS

RESULT 1
US-08-852-824-2
Sequence 2, Application US/0885282AC
Patient No. 6060272
GENERAL INFORMATION:
APPLICANT: Li et al.
TITLE OF INVENTION: Human G-protein Coupled Receptors
FILE REFERENCE: 1488,1220000
CURRENT APPLICATION NUMBER: US/08/452-824C
CURRENT FILING DATE: 1997-05-04
NAME OF SEQUENCER: 18
SCHEMA: Patent In Ver. 2.0
SEQ ID NO: 2
LENGTH: 342
TYPE: PRT
ORGANISM: genomic
US-08-852-824-2

Query Match 100.0% Score 1778; DB 3; length 342;
Best local Similarity 100.0%; Pred. No. 1,36-144;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q1	1	MOAVDNILTSAPCNISLCTRPVVFLLVYVLFVATITNGLAMFPGQTSKSNFI	60
D1	1	MOAVDNILTSAPCNISLCTRPVVFLLVYVLFVATITNGLAMFPGQTSKSNFI	60
Q2	61	IFLKNTVSLDLMLIFEFKILSLAKTSPKTFVAVISVLYETMYISIFLGITI	120
D2	61	IFLKNTVSLDLMLIFEFKILSLAKTSPKTFVAVISVLYETMYISIFLGITI	120
Q3	121	LVYGVILPKPKISNPKNIISAKHISVITWAPKPLISPNMLINKVQPKVKKSPILKS	180
D3	121	LVYGVILPKPKISNPKNIISAKHISVITWAPKPLISPNMLINKVQPKVKKSPILKS	180
Q4	181	EEGLVMEIVNIGVIMINELIYVYVITLITELYSVYRTGVKVPKKVNVVFI	240
D4	181	EEGLVMEIVNIGVIMINELIYVYVITLITELYSVYRTGVKVPKKVNVVFI	240
Q5	241	IIAVFFIVFVPHFAPIPYIISQTPVDFCTAENTLFFVKESTIMLSLNLDTLPFTYF	300
D5	241	IIAVFFIVFVPHFAPIPYIISQTPVDFCTAENTLFFVKESTIMLSLNLDTLPFTYF	300
Q6	301	LRKSFNSLISMLKCPNSAISLSLNPKKELGSDPNEETPW	342
D6	301	LRKSFNSLISMLKCPNSAISLSLNPKKELGSDPNEETPW	342

RESULT 2
US-09-221-456-2


```

ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: IBM Compatible
SOFTWARE: FASTSHO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,871
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PR-0237 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: MIM3D101
CLONE: 568987
US-08-812 871 1

Query Match 44.8%; Score 797; DB 2; Length 333;
Best Local Similarity 47.8%; Prod. No. 7.7e-61;
Matches 151, Conservative 57, Mismatches 106, Indels 2, Gaps 1;

DB 17 CTRFKITGVLPFLYVLFVGLTINLAMIIFGLSKSNFIPLKNTVSLDLMLT 76
15 CPDRIVQVLPALYVETGLTLNLALWVFIHSSSTFIYLTNTLADLIMTL 74
DB 77 FPFKILSLAKLIGCPRTFCVTSVIFPIYMWISLPLGLIIOYKIFPFKISMPK 136
75 LPEKILSLHLPQDLRAVFCFSSVIFETMYGVILGLIAPFRFLKIIFPLKNTLK 134
DB 137 NLGAKILSVIWMFELISLPNMLITNRQPRDKVKKCSFLKSEGLVWHEITVYTCOV 196
135 KIVFAKIVSIFLWFLFPLSLIPMILSNKEATPPSSVKKCASLKGPIGLKHWQVNNICOF 194
DB 197 IIVWFLVIVVYTLITKFLPSYVPTFRGVKVPKKVNVKVFITINVFITGVFHFAR 256
195 IIVWFLVIVVYTLITKFLPSYVPTFRGVKVPKKVNVKVFITINVFITGVFHFAR 254
DB 257 IIVWFLVIVVYTLITKFLPSYVPTFRGVKVPKKVNVKVFITINVFITGVFHFAR 316
255 VVTHSGTNNKTKDKLQNLFLAKETTLFLATNINCMPLISIFLCKKTEKTLPCMO--G 312
DB 317 NSATSLSDNKKKED 312
313 RKTASSQFNHSSQTD 328

```

RESULT 5
US-08-467-948A-29

Sequence 29, Application US/08467948A
Patent No. 5998164
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG

```

APPLICANT: LI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: HULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides encoding human G-protein
TITLE OF INVENTION: Coupled Receptor GPP2
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESS: STERN, KESSLER, GOLDSSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/24079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488 1140003/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
INFORMATION FOR SEQ ID NO. 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-467-948A-29

Query Match 43.4%; Score 772; DB 2; Length 325;
Best Local Similarity 47.5%; Prod. No. 1e-58;
Matches 149, Conservative 60, Mismatches 105, Indels 0, Gaps 0;

DB 6 NLTSAPNTSLTPDKITGVLPFLYVLFVGLTINLAMPITFCQIPKSNFIPLKN 65
2 NSISQPRDSQSNLLITQDIIIVLYCMVFIACILNLSGVMIFVVPSSKSPITVKN 61
DB 66 TVISDLMLIFPRKILSDAKIGCPRTFCVTSVIFPIYMWISLPLGLIIOYK 125
62 IIVWFLVIVVYTLITKFLPSYVPTFRGVKVPKKVNVKVFITINVFITGVFHFAR 121
DB 126 TTRPKTSNPKNLGAKILSVIWMFELISLPNMLITNRQPRDKVKKCSFLKSEGLV 185
122 IIVWFLVIVVYTLITKFLPSYVPTFRGVKVPKKVNVKVFITINVFITGVFHFAR 181
DB 186 WHEITVYTCOVITWFLVIVVYTLITKFLPSYVPTFRGVKVPKKVNVKVFITINVF 245
182 IIVWFLVIVVYTLITKFLPSYVPTFRGVKVPKKVNVKVFITINVFITGVFHFAR 241
DB 246 FICVPPHAPKIVYTLISQPRVFCVTSVIFPIYMWISLPLGLIIOYK 305
242 FVCFVPHIARIPTTKQTEAHNSQSKETIRYKETTLLISANVCLDPIITFFLQDP 301
DB 306 NNSLSIMKCPNSA 319
302 REILCKKIHLPLKA 315

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QY 186 WHFIVNYICGVLPWLNFLIVCYTLLTKETRSYVRTRGVCKVPRKKYVAVFIIIAVF 245
 DB 183 MIKASNYIVAIWFIWFLIIYFYTATITKIKRSILKSSRNSTSYKKKSSRNIFSIIVEF 242
 QY 246 FICFVDPFHARIPYTLISQTRDVFDCIAENTLFEVKESTLMTLSNACLDPIFYFLCKSF 305
 DB 243 FVCFVYHIAIRIPYTKSQTRFAHYSQSKRLRYMKRFTLLISAANVCIDPIIYFPLCGVF 302
 QY 306 RNSLISMLKCPNSA 319
 DB 303 RELCKCKLHPLKA 316

RESULT 8

US-09-303-524A-2
 ? Sequence 2: Application US/09303524A
 ? Patent No. 6218873
 ? GENERAL INFORMATION:
 ? APPLICANT: CHAMBERS, JONATHAN K.
 ? APPLICANT: STEWART, BRIAN R.
 ? APPLICANT: AMES, ROBERT S.
 ? APPLICANT: SAKAO, HENRI M.
 ? APPLICANT: FOLEY, JIM
 ? APPLICANT: ARNOLD, ANNE ROMANIC
 ? TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
 ? TITLE OF INVENTION: ANTAGONISTS OF THE INTERACTION BETWEEN THE HUMAN KIAA0001
 ? TITLE OF INVENTION: RECEPTOR AND LIGANDS THEREOF
 ? FILER REFERENCE: G950007
 ? CURRENT APPLICATION NUMBER: US/09/303,524A
 ? CURRENT FILING DATE: 1999-04-30
 ? PRIOR APPLICATION NUMBER: 60/083,967
 ? PRIOR FILING DATE: 1998-05-01
 ? NUMBER OF SEQ ID NOS: 2
 ? SOFTWARE: FASTSEQ for Windows Version 3.0
 ? SEQ ID NO 2
 ? LENGTH: 338
 ? TYPE: FRT
 ? ORGANISM: Homo sapiens
 US-09-303-524A-2

Query Match 43.4%; Score 772; DB 4; Length 338,
 Best Local Similarity 47.5%; Pred. No. 1,1e-58;
 Matches 149; Conservative 60; Mismatches 105; Indels 0; Gaps 0;

QY 6 NLTSAGCNISLCTRYKKITGVLPPLIYTVLFWGLITNGLAMKIFVQIRKSNHIFLILKN 65
 DB 3 NNTSTQPHBSCSONLITIQIIVLYCWFPIAGIILNGVSGMIFPYVSSKSFIIYILKN 62
 QY 66 TVISDLMLITPEFKILSDAKIATPPLRTFVGVVTSVIFYFTMYLISISPLGLITIDRYOK 125
 DB 63 IVIADVMSITPEFKITLIGSGQPMQOLANVFCVSAVLPYVMYVSIIVPFGILISDRYVK 122
 QY 126 TTRPFTSNRNKILGAKILSVIWAAPHLISLPMMLITNRQPRKNVKKCSFLKSEFGLV 185
 DB 123 IYKPLTSTFLOSYSKSLSVIWMMLLLELAVPNIITLNGSVFVQIGCTELKSEIAGPK 182
 QY 186 WHFIVNYICGVLPWLNFLIVCYTLLTKETRSYVRTRGVCKVPRKKYVAVFIIIAVF 245
 DB 183 MIKASNYIVAIWFIWFLIIYFYTATITKIKRSILKSSRNSTSYKKKSSRNIFSIIVEF 242
 QY 246 FICFVDPFHARIPYTLISQTRDVFDCIAENTLFEVKESTLMTLSNACLDPIFYFLCKSF 305
 DB 243 FVCFVYHIAIRIPYTKSQTRFAHYSQSKRLRYMKRFTLLISAANVCIDPIIYFPLCGVF 302
 QY 306 RNSLISMLKCPNSA 319
 DB 303 RELCKCKLHPLKA 316

RESULT 9

US-08-988-876-3
 ? Sequence 3: Application US/08988876
 ? Patent No. 6063596
 ? GENERAL INFORMATION:
 ? APPLICANT: Lal, Preeti
 ? APPLICANT: Bandman, Olga
 ? APPLICANT: Hillman, Jennifer L.
 ? APPLICANT: Yoo, Henry
 ? TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
 ? TITLE OF INVENTION: WITH IMMUNE RESPONSE
 ? NUMBER OF SEQUENCES: 9
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESS: Incyte Pharmaceuticals, Inc.
 ? STREET: 3174 Porter Drive
 ? CITY: Palo Alto
 ? STATE: CA
 ? COUNTRY: USA
 ? ZIP: 94304
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Diskette
 ? COMPUTER: IBM Compatible
 ? OPERATING SYSTEM: DOS
 ? SOFTWARE: FASTSEQ for Windows Version 2.0
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/988,876
 ? FILING DATE: Herewith
 ? CLASSIFICATION:
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER:
 ? FILING DATE:
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Hillings, Lucy J.
 ? REGISTRATION NUMBER: 36,749
 ? REFERENCE/DOCKET NUMBER: PR-0441 US
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: 650-855-0555
 ? TELEFAX: 650-845-4166
 ? TELEX:
 ? INFORMATION FOR SEQ ID NO: 3:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 358 amino acids
 ? TYPE: amino acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? IMMEDIATE SOURCE:
 ? LIBRARY: PROSTUT09
 ? CLONE: 1650519
 US-08-988-876-3

Query Match 38.2%; Score 679.5; DB 3; Length 358;
 Best Local Similarity 43.7%; Pred. No. 9e-51;
 Matches 132; Conservative 64; Mismatches 99; Indels 7; Gaps 4;

QY 6 NLTSAGCNISLCTRYKKITGVLPPLIYTVLFWGLITNGLAMKIFVQIRKSNHIFLILKN 64
 DB 25 NNSDGRKGNNTL---HNEFDITVLPVLIITFVASILNLGLAVIFEHIPKTSFIEYIK 81
 QY 65 NTVISDLMLITPEFKILSDAKIATPPLRTFVGVVTSVIFYFTMYLISISPLGLITIDRYOK 124
 DB 62 NIVVADLIMLITFPFRIVHDAGFGWYKFIIDKRTSVLPYANMYISVPLGLISIDRYL 141
 QY 125 KTRPFTSNRNKILGAKILSVIWAAPHLISLPMMLITNRQPRKNVKKCSFLKSEFGLV 184
 DB 142 KVVKFGDSRMYSITFTKVLSSCVWVIAVLSLPIILINQPTEDNIDHCKSLKSPGLV 201
 QY 185 WHFIVNYICGVLPWLNFLIVCYTLLTKETRSYVRTRGVCKVPRKKYVAVFIIIAVF 243
 DB 202 KMTAVTVNSCLFVAVLVILIGYIATSRTHKS--SRQFTSOSKRRKINOSTIRVVA 259
 QY 244 VFIICVDPFHARIPYTLISQTRDVFDCIAENTLFEVKESTLMTLSNACLDPIFYFLCKSF 303
 DB 260 VYFCGLPIYHICRMDSITPSHLDRIIDBSAQKIVYCKRFTLLISAANVCIDPIIYFPLCGVF 319

QY 197 FMINPLIVVCTLLPKK-----LVKSVYRTGKGVPRKVVNKFV111IAVFIICPV- 251
 DB 195 FMVIVLILVYVYVIAKKYMLIESPKVTEKTKSMWAKYLLSLMSLCVLLHFISPE 254
 QY 252 PPRARIPVTLISQTRVNDIAENTLHYVKESTLW 285
 DB 255 FMHIVKPTIKLT---VDCR-NCCLLKKOISFW 284

RESULT 12

US-08-702-344-28

Sequence 28, Application US/08702344

Patent No. 5723415

GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth

APPLICANT: McCoy, John

APPLICANT: Lavallie, Edward

APPLICANT: Hodge, Lisa

APPLICANT: Merberg, David

APPLICANT: Treacy, Maurice

APPLICANT: Spaulding, Vikki

TITLE OF INVENTION: SEVERED PROTEINS AND POLYPEPTIDES

TITLE OF INVENTION: ENCODING THEM

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/702,344

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 319 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-702-344-28

Query Match 27.4%; Score 488; DB 1; Length 319;

Best local Similarity 34.5%; Pred. No. 1.8e-34;

Matches 112; Conservative 62; Mismatches 125; Indels 26; Gaps 9;

QY 13 NMSICTRNYKIGVIFPLIVLPEVGLITNGCLAMRIFFQIRSKSNFI-IFLKNVVISDL 71
 DB 3 NNSFFGVYKQLEP-FTYFFLVFLVGLISGCFATMAFIKNTNDRVCYSITLILNLADF 61
 QY 72 IMLITFPKLLSDAKIGCP--LKITVGVSVIIFPTMYISISLGLITIDRYOKTRP 129
 DB 62 LILHAIPIKVIIVD--IGVAPWKIKLIFHCQVACLIIYINMYISILIFLAVSIDKCIQTHS 119
 QY 130 FRTSPKMLLAKILSYVIAFMELSLPNMLITNRQPKDNVKKCSPLKSEFGIWMHEI 189
 DB 120 KTVIPIQPCFAKMISTVWMLVAILIIVPNMIPKIDIKSKSNVCCMFKKCFGRNNHLL 179

QY 190 VNIICQVIFMIN-ILIVVCTLLITKELYSVYRTGKGVPR-KKVVNKFV111IAVF1 247
 DB 180 TNFICVAF-LNFSAILIISNCVIRQIRN-----KQENPNPKKLLINLLVLTGY11 234
 QY 248 GEPFHFARIPVTLISQTRVNDIAENTLHYVKESTLW1SLACDPFIYFLKSFEN 307
 DB 235 GEPFHFARIPVTLISQTRVNDIAENTLHYVKESTLW1SLACDPFIYFLKSFEN 294
 QY 308 SLI-----SMLKCPNSA 319
 DB 295 KVTETASPKEKKAKEKLCENNA 319

RESULT 13

US-08-118-270-39

Sequence 39, Application US/08118270

Patent No. 5508384

GENERAL INFORMATION:

APPLICANT: Murphy, Randall H.

APPLICANT: Schuster, David I.

TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN

TITLE OF INVENTION: PREPEPTIDS, AND COMPOSITIONS AND METHODS THEREOF

NUMBER OF SEQUENCES: 348

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEWMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/118,270

FILING DATE: 09-SEP-1993

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 07/943,236

FILING DATE: 10-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Townsend, Kevin G.

REGISTRATION NUMBER: 34,033

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 326 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-118-270-39

Query Match 23.1%; Score 410.5; DB 1; Length 326;

Best local Similarity 32.2%; Pred. No. 7.7e-28;

Matches 106; Conservative 65; Mismatches 137; Indels 21; Gaps 9;

QY 27 LPELITVLPFGVLTNGMLAMRIFFQIRSKSNFI-IFLKNVVISDLMLTFPKLSD 84
 DB 1 LPLIVSILIFVIGLIANGYVIAVFAIRYSKKNFIKIFVNLIVADILFLITPLIMVYV 60
 QY 85 AKIGTGLPFPVGVSVIIFPTMYISISLGLITIDRYOKTRPPTSIPKMLDAKIL 144
 DB 61 SNGSNMFLKFLCNGGLFFINITYSVAFGLVITTFQAVKYPFKTQVATRRGIAL 120
 QY 145 SVVITW-----AFMFLSLIPNMILITNRQPKDNVKKCSPLKSEFGIWMHEI 194
 DB 145 SVVITW-----AFMFLSLIPNMILITNRQPKDNVKKCSPLKSEFGIWMHEI 194



RESULT	1
AA081576	
ID	AA081576, standard, Protein; 342 AA.
XX	
AC	AA081576;
XX	
L1	22-FEB-1999 (first entry)
XX	
DE	EBV-Induced G-protein coupled receptor (EBI-2) polypeptide.
XX	
XX	EBV-Induced G-protein coupled receptor; EBI-2; Epstein-Barr Virus; ulcer
KW	endothelium; differentiation gene; PDG1-like G protein coupled receptor;
KW	recombinant, agonist, asthma, Parkinson's disease, heart failure, asthma;
KW	hypotension; urinary retention; osteoporosis; antagonist; hypertension;
KW	angina pectoris; myocardial infarction; allergy, psychosist; depression;
KW	migraine; vomiting; stroke; eating disorder;migraine headache; cancer;
XX	prostatic hypertrophy; detection; drug screening.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
EH	Misc-difference 6
ET	/note- "encoded by ATT"
FT	Misc-difference 14
FT	/note- "encoded by AAC"
XX	
PN	MO9850549-A2.
XX	
ED	12-NOV-1998.
XX	
XX	
XX	07-MAY-1998; 98WD-US09048.
XX	
XX	07-MAY-1997; 97MS-0852824.
XX	

(HOMA) HUMAN GENE: SCL 1NC.

LI Y. Rubin SM.

WPI: 1999 034722/03.

N-PSDB: AAV99760.

New isolated human G protein coupled receptors used to develop products for treating e.g. asthma, Parkinson's disease, heart failure, osteoporosis, hypertension, psychosis, eating disorders or cancer.

claim 1: Fig 1A-C, 63pp; English.

This represents a EHV induced G-protein coupled receptor (EHI-2) polypeptide. The encoding DNA is deposited under the accession number ADCC No. 200004. The invention provides two human G-protein coupled receptor polypeptides, the polypeptides are human Epstein-Barr Virus (EBV) induced G protein coupled receptor, designated EHI-2 polypeptide and a human endonuclease differentiation gene (EHC) like G-protein coupled receptor, designated EHI-1 like G-protein coupled receptor. Vectors comprising the EHI-2 and EHI-1 like polypeptides encoding DNA can be used to transform host cells for the recombinant production of the proteins. Agonists for G-protein coupled receptors can be used for the treatment of asthma, Parkinson's disease, acute heart failure, hypertension, urinary retention and osteoporosis. Antagonists can be used for the treatment of hypertension, anxiety disorders, myocardial infarction, ulcers, asthma, allergies, psychosis, depression, migraine, vomiting, stroke, eating disorders, migraine headaches, cancer and benign prostatic hypertrophy. The products can also be used for detection, diagnosis and drug screening.

Sequence 642 AA:

Query Match 100.0%; Score 1778; DH 20; Length 342;

Best Local Similarity 100.0%; Pred. No. 4, 20-187;

Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

AAV71306 AAV71306 standard; protein; 342 AA.

AAV71306 AAV71306

02 NOV 2000 (first entry)

Human orphan G protein coupled receptor hGHRB.

Human, orphan G protein coupled receptor: GPCR, hGHRB; drug screening; transmembrane receptor; expressed sequence tag; EST; signal cascade.

Homo sapiens.

WO200011258-A2.

02-JUN-2000.

13-OCT-1999; 99WO 0523687.

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20-NOV-1998; 98US-0109213.
16-FEB-1999; 99US-0120416.
26-FEB-1999; 99US-0121852.
12-MAR-1999; 99US-0123946.
12-MAR-1999; 99US-0123949.
28-MAY-1999; 99US-0136436.
28-MAY-1999; 99US-0136437.
28-MAY-1999; 99US-0136439.
28-MAY-1999; 99US-0136567.
28-MAY-1999; 99US-0137127.
28-MAY-1999; 99US-0137131.
29-JUN-1999; 99US-0141448.
29-SEP-1999; 99US-0156555.
29-SEP-1999; 99US-0156634.
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29-SEP-1999; 99US-0156653.
01-OCT-1999; 99US-0157280.
01-OCT-1999; 99US-0157281.
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01-OCT-1999; 99US-0157293.
01-OCT-1999; 99US-0157294.
12-OCT-1999; 99US-0417044.
12-OCT-1999; 99US-0417044.

```

(AREN-) ARENA PHARM INC.

Chen R, Dang HT, Liaw CM, Lin I;

WPI: 2000-40068/34.

N-PSDB: AAD01133.

Novel human orphan G protein coupled receptors and the encoding cDNAs for use in the identification of G protein-coupled receptor agonists.

Claim 62; Page 82-83; 102pp; English.

The present amino acid sequence is the hGHRB, an endogenous human orphan G protein-coupled receptor (GPCR), expressed in left and right cerebellum, kidney and lung. The hGHRB cDNA was identified using full length EST (expressed sequence tag) 764455 as a probe. The orphan GPCR of the invention, like all GPCRs has seven transmembrane alpha helices with an extracellular N terminus and an intracellular C-terminus. However, no endogenous ligands has yet been identified for the proteins of the invention. The orphan GPCRs may be used in the identification of their endogenous ligands, and to screen potential GPCR agonists and antagonists for use as pharmaceutical agents. The proteins may also be used in the study of GPCR-mediated signalling cascades, and to elucidate their precise role in normal and diseased human conditions. Nucleic acid encoding human orphan GPCRs may be used for tissue localisation expression analysis to provide information about their function in healthy and pathological states.

Sequence 342 AA:

Query Match 100.0%; Score 1778; DH 21; Length 342;

Best Local Similarity 100.0%; Pred. No. 4, 20-187;

Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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50 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
51 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
52 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
53 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
54 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
55 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
56 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
57 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
58 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
59 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
60 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
61 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
62 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
63 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
64 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
65 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
66 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
67 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
68 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
69 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
70 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
71 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
72 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
73 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
74 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
75 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
76 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
77 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
78 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
79 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
80 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
81 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
82 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
83 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
84 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
85 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
86 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
87 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
88 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
89 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
90 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
91 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
92 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
93 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
94 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
95 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
96 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
97 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
98 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
99 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60
100 I mpsvnhit sapgnt slct rdyk tgy lfp lly vltv lfnq lamr tfg rsksnfi 60

```



```

Db      1 mgavdhltisapntslctrdykitqylfpllytvlffvgtlenglamrffqitrsnft 60
QY      61 IFLKNTVLSULMLITFFPKITSEAKLSTGPILEFWVGVTSVFEFTMYISISFLITL 120
Db      61 IILKOLVSDLLMLITLPIKLSDAKLGPIPLTTCVGLSVLYLTMISISLIGLIT 120
QY      121 DRYQKTRPPKTSNPKNI:CAKILSVIWAHPFLSLNMLITNRQPRDKVKKCSPLKS 180
Db      121 dryqkltrpkiisnpknliyakilsvlwafmlislpmillnrpdrkknvkkcsfiks 180
QY      181 EFLVMEHLVNTICQVIFMNFIVVCTLTITKELRSVVTPTVGVKPKKRVKVVVFT 240
Db      181 eglvwhelvtgvytfcvifmfvctltitkclrsyvtltvgkvpkkvkvvft 240
QY      241 IIAVFICVPHFARIPYTLISQTRDVPCTAENTLFVVKESTIMWTSLNACLDPITFF 300
Db      241 IIAVFICVPHFARIPYTLISQTRDVPCTAENTLFVVKESTIMWTSLNACLDPITFF 300
QY      301 ICKSPRNSLSIMKCPNSATSISQDNRRKKRQDGNPNEETPM 342
Db      301 ICKSPRNSLSIMKCPNSATSISQDNRRKKRQDGNPNEETPM 342

RESULT 3
AA02840
ID      AA02840 standard; Protein; 342 AA.
AC      AA02840:
XX
XX      22-AUG-2000 (first entry)
DE      Human G protein-coupled receptor hGHR8 protein SEQ ID NO:34.
XX
XX      Human G protein-coupled receptor; GPCR; transmembrane receptor;
KM      Identification; agonist; screening; therapeutic; pharmaceutical;
KW      mutant.
XX
XX      Homo sapiens.
OS
XX
XX      W0200022131 A2
PN
PD      20-APR-2000.
XX
XX      13-OCT-1999; 99WO-US24065.
XX
XX      13-OCT-1999; 99US-0170446.
PR      12-NOV-1998; 99US-016029.
PR      20-NOV-1998; 99US-0109213.
PR      27-NOV-1998; 99US-0110060.
PR      16-FEB-1999; 99US-0120416.
PR      26-FEB-1999; 99US-0121862.
PR      12-MAR-1999; 99US-0123944.
PR      12-MAR-1999; 99US-0123945.
PR      12-MAR-1999; 99US-0123946.
PR      12-MAR-1999; 99US-0123949.
PR      12-MAR-1999; 99US-0123951.
PR      28-MAY-1999; 99US-0136437.
PR      28-MAY-1999; 99US-0136439.
PR      28-MAY-1999; 99US-0137127.
PR      28-MAY-1999; 99US-0137131.
PR      28-MAY-1999; 99US-0137567.
PR      10-JUN-1999; 99US-0141448.
PR      27-AUG-1999; 99US-0151114.
PR      03-SEP-1999; 99US-0152524.
PR      29-SEP-1999; 99US-0156633.
PR      29-SEP-1999; 99US-0156655.
PR      29-SEP-1999; 99US-0156634.
XX
XX      (AREN-) ARENA PHARM INC.
PA
XX
PI      Behan DJ, Lehmman Huiusma K, Chalmers DJ, Chen K, Bang H;

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PI      Gore M, Liaw CW, Lin L, Howitz K, White G;
XX
XX      WP1: 2990-317986/27.
DR      N-PSDB: AAA46034.
XX
XX      Non-endogenous, human G protein-coupled receptors for screening
PT      receptor, inverse or partial agonists useful as therapeutic agents
XX
XX      Example 1: Page 112-113; 187pp; English.
PS
XX
XX      The present invention describes transmembrane receptors, preferably
CC      human G protein coupled receptors (GPCR), for which the endogenous
CC      ligand is unknown (orphan GPCR receptors). More specifically the present
CC      invention relates to non-endogenous, constitutively activated versions
CC      of a human GPCR. These non-endogenous human GPCRs can be useful for
CC      the direct identification of candidate compounds as receptors agonists,
CC      inverse agonists or partial agonists for use as pharmaceutical agents.
CC      AAA46017 to AAA46126 and AA02845 to AA02859 represent sequences used in
CC      the exemplification of the present invention.
XX
XX      Sequence 342 AA:
SQ
XX

Query Match      100.0%; Score 1778; DB 21; Length 342;
Best Local Similarity 100.0%; Ident. No. 4; 187;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MQAVDNLTSAPGNTSLCTRDYKITQVIFPLLYTLEFGITNGLAMRIFPOIRSKSNFT 60
Db      1 mgavdhltisapntslctrdykitqylfpllytvlffvgtlenglamrffqitrsnft 60
QY      61 IFLKNTVLSULMLITFFPKITSEAKLSTGPILEFWVGVTSVFEFTMYISISFLITL 120
Db      61 IILKOLVSDLLMLITLPIKLSDAKLGPIPLTTCVGLSVLYLTMISISLIGLIT 120
QY      121 DRYQKTRPPKTSNPKNI:CAKILSVIWAHPFLSLNMLITNRQPRDKVKKCSPLKS 180
Db      121 dryqkltrpkiisnpknliyakilsvlwafmlislpmillnrpdrkknvkkcsfiks 180
QY      181 EFLVMEHLVNTICQVIFMNFIVVCTLTITKELRSVVTPTVGVKPKKRVKVVVFT 240
Db      181 eglvwhelvtgvytfcvifmfvctltitkclrsyvtltvgkvpkkvkvvft 240
QY      241 IIAVFICVPHFARIPYTLISQTRDVPCTAENTLFVVKESTIMWTSLNACLDPITFF 300
Db      241 IIAVFICVPHFARIPYTLISQTRDVPCTAENTLFVVKESTIMWTSLNACLDPITFF 300
QY      301 ICKSPRNSLSIMKCPNSATSISQDNRRKKRQDGNPNEETPM 342
Db      301 ICKSPRNSLSIMKCPNSATSISQDNRRKKRQDGNPNEETPM 342

RESULT 4
AA94444
ID      AA94444 standard; Protein; 342 AA.
XX
XX      AA94444:
AC
XX
XX      21-AUG-2000 (first entry)
DT
XX
XX      Human 15625 receptor protein.
DE
XX
XX      Human; G-protein-coupled receptor; GPCR; 15625 receptor protein;
KM      glial cells; spleen; colon; liver; brain; T-cell; heart;
KM      red cell; thymus; B-cell; pancreas; disordered; chromosome 3;
KM      anemia, neutropenia; thrombocytopenia, gene therapy; ss.
XX
XX      Homo sapiens.
OS
XX
XX      Key Location/Qualifiers
FH      1..25
FT      Domain
FT      Modified-site 6..9

```

FT /label= N-allycosylation
 FT Misc difference 13
 FT /label= "Encoded by AGC"
 FT 13..16
 FT Modified site
 FT /label= N-allycosylation
 FT 26..402
 FT Domain
 FT /label= Transmembrane-domain
 FT 49..44
 FT Modified site
 FT /label= N-myristoylation
 FT 121..123
 FT Modified site
 FT /label= GPCR signal transduction site
 FT 126..128
 FT Modified site
 FT /label= protein_kinase_C_phosphorylation
 FT 161..165
 FT Modified site
 FT /label= protein_kinase_C_phosphorylation
 FT 174..176
 FT Modified site
 FT /label= protein_kinase_phosphorylation
 FT 403..442
 FT Domain
 FT /label= Intracellular-domain
 FT 404..406
 FT Modified site
 FT /label= protein_kinase_C_phosphorylation
 FT 341..348
 FT Modified site
 FT /label= N-myristoylation

W0200028028 A1

18 MAY 2000.

05 NOV 1999; 99WD-0825956.

06 NOV 1998; 98WS-0187134.

25 AUG 1999; 99OS-0182918.

(MILL.) MILLENNIUM PHARM INC.

Glucksmann MA, Gu W, Welch NS;

WPI: 2000 476543/42.

N-PSDB: AAA27126.

Identifying an agent modulating the level or activity of G-protein coupled receptor useful for screening a cell derived from a subject having disorders such as anorexia, neutropenia and thrombocytopenia -

Disclosures: Page 88 89; 97pp; English.

The present sequence shows the 15625 receptor protein. It is a novel G coupled protein receptor (GPCR). The cDNA for this protein was isolated by screening a human cDNA library with sequences homologous to other GPCRs. The 15625 receptor protein is expressed in the glial cells of the brain. It is also expressed in several other tissues. The 15625 receptor protein may be useful for producing antibodies which can be used to detect the presence of the receptor protein. The 15625 receptor protein polynucleotides are useful for generating probes, primers and antisense constructs. The polynucleotides encoding the 15625 receptor proteins can also be inserted into vectors to be used in gene therapy. The disorder that may be treated using the 15625 receptor protein polynucleotides and polypeptides include anorexia, neutropenia and thrombocytopenia.

XX Sequence 442 AA;

Query Match 100.0%; Score 1778; DH 21; Length 342;

Best Local Similarity 100.0%; Prod. No. 4.2e-187;

Matches 442; Conserved 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOAVALNTSACNCTSLPQKTKITGVLFPLVYVLFVGLITKGLAMRIFQIRSKNFI 60
 DB 1 MGVAVNTSACNCTSLPQKTKITGVLFPLVYVLFVGLITKGLAMRIFQIRSKNFI 60
 QY 61 IETKNTVLSQMLITFPRKILISPAKLGTPLEFVGVYTVSVIFETWYISIFGLIT 120
 DB 1 IETKNTVLSQMLITFPRKILISPAKLGTPLEFVGVYTVSVIFETWYISIFGLIT 120

DB 61 IILKVLTSdlmlllfpiklsdaklqplrlivcqvtsvlylmvysilqltli 120
 QY 121 DRYOKTTPRPKTSNPKNIGAKILSVIWAHFWLISLNMILTRNRPDKVKKCSPLKS 180
 DB 121 dYgKtTpRfKtsnpKniGakIlsvIwAhfWlIsLnmIlTrnRpDkVkkCsPlKs 180
 QY 181 EFGLVWHEIVNYTCOVTFWNIPLIVIVCYTLITKELYSYVTRGVKVPKKYVWYFI 240
 DB 181 efglvwheivnytcovtfwniplivivcytlitkelysyvtrgvkvppkkyvfi 240
 QY 241 ITAVPFICVPHFAPARIPYTLISQTRVPCVAKNLFYVKSSTIMLTSIACIDPITPF 300
 DB 241 itavpficvphfaparipytlisqtrvpcvaknlfyvksstimltsiacdipitpf 300
 QY 301 ICKSPKNSLISMICKNSATSLSDPNKKKKFDQCGDPNFEETPM 342
 DB 301 IckSpKnsLIsMICKnSAtSlSdPNKKKKfDqCGDPNFEETpm 342

RESULT 5

AAW79249

ID AAW79249 standard; Protein; 342 AA.

XX AAW79249;

DT 06-NOV-2001 (first entry)

DE Human protein SEQ ID NO 1911.

KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;

KW vaccine; peptide therapy; stem cell growth factor; hematopoiesis;

KW tissue growth factor; immunomodulatory; cancer; leukemia;

KW nervous system disorder; arthritis; inflammation.

OS Homo sapiens.

PN W0200157190-A2.

PD 09-AUG-2001.

PF 05-FEB-2001; 2001WO-0504098.

PR 03-FEB-2000; 2000US-0446914

PR 27-APR-2000; 2000US-0560875

PR 20-JUN-2000; 2000US-0536075.

PR 19-JUL-2000; 2000US-0620325.

PR 01-SEP-2000; 2000US-0654936.

PR 15-SEP-2000; 2000US-0664561.

PR 20-OCT-2000; 2000US-0694325

PR 30-NOV-2000; 2000US-0728422.

PA (HSE-) HYSEQ INC.

PI Tang YT, Liu C, Dermanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;

PI Zhao QJ, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;

PI Xue AJ, Yang Y, Wei human T, Goodrich R;

WPI: 2001 476283/51.

N-PSDB: AAK52382.

PT Nucleic acids encoding polypeptides with cytokine-like activities,

PT useful in diagnosis and gene therapy -

PS Claim 20; Page 4310, 6221pp; English.

CC The invention relates to polynucleotides (AAK51456-AAK54435) and the
 CC encoded polypeptides (AAW78323-AAW80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and

CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO: 210 (AAK52561), 211 (AAK52582) and 266
 CC (AAK6020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.

XX Sequence 342 AA:

Query Match 100.0%; Score 1778; DB 22; Length 342;
 Best Local Similarity 100.0%; Pred. No. 4, 2e-187;
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOAVDNLTAPKNTSLCTDQYKLTQVLPFLTYTLFVGLINGLARIFFQIRSKSNFI 60
 DB 1 mqvadnltsapgnslctrdykltqytlfpfylvtfvgtlmgamtrffqtrsksnfi 60
 QY 61 IFLKNTVISDLMLLTPFPKILSDAKLCTGCPKRTFVCQVTSVFFPYMYISISFLGLTI 120
 DB 61 iflknvisdlmltltpfpkilsdaklctgcpkrtfvcqvtsvffpymyisisflgliti 120
 QY 121 DRYQKTRFPFKTSNPKNLGAKILSVIWMFELSLDPNMLITNRPDKKVKKCSFLKS 180
 DB 121 dryqktrfpfktsnpknllgakisvviwmfelsldpnmlltnrpdckvkksflks 180
 QY 181 EFGIWMHEIVNYIGVIFMINFLIVCYTLITKELYSYVPTGCVKPKKVVKKVFI 240
 DB 181 efgiwmheivnyigvifminflivcytlitkelysyvptgcvkpkkvkvvkvi 240
 QY 241 IIAVFICTVPPHFAPIPYTLNTRGVFMTAFENTLFYVKESTLWLTJSLNCLDEPIYFF 300
 DB 241 iiavfictvpphfaripytlntgrvfmrtafentlfyvkfstlwltjslncldpiyiff 300
 QY 301 ICKSFHNSIISMICKPNSATSLSDQNRKKRQDGPNEETPM 342
 DB 301 icksfhnsiismickpnsatslsdqnrkkrqdgpneetpm 342

RESULT 6
 AAE04386
 ID AAE04386 standard: Protein: 342 AA
 XX
 AC AAE04386;
 XX
 DT 04-SEP-2001 (first entry)
 XX
 DE Human P2-purineric receptor subtype, P2Y12.
 XX
 XX Human P2-purineric receptor subtype, P2Y12, standard, vasodilator, thrombolytic,
 XX cerebroprotective, gynaecological, ADP, adenosine 5'-diphosphate, angina,
 XX myocardial infarction, ischaemic attack, preclampsia, bleeding disorder;
 XX carotid endarterectomy; vascular graft surgery; brain disorder; migraine;
 XX vascular injury; schizoidism; eating disorder; depression; anorexia;
 XX peripheral vascular disease; platelet aggregation; restenosis; embolism;
 XX thromboembolic purpura; stroke; pertussis toxin-sensitive G protein;
 XX G1; disseminated intravascular coagulation; thrombosis.
 XX
 OS Homo sapiens.
 XX
 XX
 FI Key Location/Qualifiers
 FT Domain 27..50 /label= Transmembrane_domain_1
 FT 58..82 /label= Transmembrane_domain_2
 FT 97..121 /label= Transmembrane_domain_3
 FT 140..164 /label= Transmembrane_domain_4
 FT 189..213 /label= Transmembrane_domain_5
 FT 234..259 /label= Transmembrane_domain_6
 FT Domain /label= Transmembrane_domain_6

FT Domain 278..303
 FT /label= Transmembrane_domain_7

LN WJ200146454-A1

PD 28-JUN-2001.

FF 26-DEC-2000; 2000MO-US34998.

PR 23-DEC-1999; 99US-0171622.

PA (PPT-1) COR THERAPEUTICS INC.

PI Conley PB, Jantzen H, Ramakrishnan-Dubridge V, Julius DJ;

DR Holloper G;

UK W11: 2001-41808-444.

DR N-PSDB; AAD08695.

PT Novel isolated ADP receptor, termed P2Y12 receptor polypeptide, useful
 for identifying binding partners and for diagnostic applications

PS Example 1; Fig 5A; 108pp; English.

CC The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed
 CC as P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor is
 CC the subtype of P2-purineric receptor. The P2Y12 receptor is expressed
 CC selectively in the platelets and brain, and couples to a pertussis toxin
 CC sensitive G protein (G_i). P2Y12 receptor is a G protein coupled receptor
 CC that responds to ADP. The invention also relates to a method for
 CC identifying an agent which is useful for modulating acute myocardial
 CC infarction, unstable angina, chronic stable angina, transient ischaemic
 CC attacks, strokes, peripheral vascular disease, preclampsia, deep venous
 CC thrombosis, embolism, disseminated intravascular coagulation, thrombotic
 CC thrombocytopenic purpura or a bleeding disorder; thrombotic and
 CC restenosis complications following angioplasty, carotid endarterectomy,
 CC post CABG (coronary artery bypass graft) surgery, vascular graft surgery,
 CC stent placements or insertion of endovascular devices and prostheses.
 CC P2Y12 receptor is useful for identifying binding partners and for
 CC diagnostic applications. P2Y12 receptor provides targets for screening
 CC synthetic small molecules and combinatorial or naturally occurring
 CC compound libraries to regulate platelet aggregation, vascular injury, or
 CC disease as well as schizoidism, eating disorders, depression, migraine
 CC and other brain disorders. The present sequence is human P2-purineric
 CC receptor subtype, referred as P2Y12.

CC Sequence 342 AA:

Query Match 100.0%; Score 1778; DB 22; Length 342;

Best Local Similarity 100.0%; Pred. No. 4, 2e-187;

Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOAVDNLTAPKNTSLCTDQYKLTQVLPFLTYTLFVGLINGLARIFFQIRSKSNFI 60
 DB 1 mqvadnltsapgnslctrdykltqytlfpfylvtfvgtlmgamtrffqtrsksnfi 60
 QY 61 IFLKNTVISDLMLLTPFPKILSDAKLCTGCPKRTFVCQVTSVFFPYMYISISFLGLTI 120
 DB 61 iflknvisdlmltltpfpkilsdaklctgcpkrtfvcqvtsvffpymyisisflgliti 120
 QY 121 DRYQKTRFPFKTSNPKNLGAKILSVIWMFELSLDPNMLITNRPDKKVKKCSFLKS 180
 DB 121 dryqktrfpfktsnpknllgakisvviwmfelsldpnmlltnrpdckvkksflks 180
 QY 181 EFGIWMHEIVNYIGVIFMINFLIVCYTLITKELYSYVPTGCVKPKKVVKKVFI 240
 DB 181 efgiwmheivnyigvifminflivcytlitkelysyvptgcvkpkkvkvvkvi 240
 QY 241 IIAVFICTVPPHFAPIPYTLNTRGVFMTAFENTLFYVKESTLWLTJSLNCLDEPIYFF 300
 DB 241 iiavfictvpphfaripytlntgrvfmrtafentlfyvkfstlwltjslncldpiyiff 300

6) It is not sufficient to have a good idea of what you want to do. You must also have a plan of how to do it.

CC restenotic complications following angioplasty, carotid endarterectomy, and CABG (coronary artery bypass graft) surgery.

XX 6 protein coupled receptor; GPCR; MP-10 receptor; rat; CNS;
 KW central nervous system; spleen; anesthetic; analgesic.
 XX
 XX Rattus sp
 XX W020004454-A1
 XX 15 JUN 2000
 XX 08 DEC 1999; 99WO/5802402.
 XX 10 DEC 1998; 98SP/0004774
 XX (ASTR) ASTRA PHARMA INC.
 XX (ASTR) ASTRA AB
 XX Ahmad S, Holbert C, Lembo P, O'Donnell D, Walker P;
 XX Wt1; 2000 441276/47;
 XX N PSDB: AAA86042.
 XX Novel G protein coupled receptor, MP-10 receptor, useful for
 XX identification of new anesthetic and analgesic agents -
 XX
 XX Claim 1: Fig 2; 28pp; English.
 XX
 XX The present sequence is rat MP-10 receptor protein. The DNA encoding
 XX this protein was identified from a rat brain stem/spinal cord cDNA
 XX library. In situ hybridization analysis showed that MP-10 receptor
 XX mRNA is expressed diffusely but ubiquitously in the adult rat central
 XX nervous system (CNS). The mRNA was also found in adult rat spleen.
 XX MP-10 receptor protein contains several structural features
 XX characteristic of a G protein coupled receptor (GPCR). MP-10
 XX receptor protein is useful for identifying new anesthetic and analgesic
 XX agents. Such agents may be identified using assays designed to
 XX detect agonists or antagonists capable of binding to the receptor,
 XX therefore modulating intracellular signalling.
 XX
 XX Sequence: 487 AA.

Query Match 84.0%; Score 1493.5; DB 21; Length 487;
 Best Local Similarity 86.4%; Pred. No. 15;
 Matches 287; Conservative 17; Mismatches 23; Indels 5; Gaps 1;
 6 NLSAQNINSEKRRITGVHLYLVVGLINCLAMPFQIRKSNF11PLKN 65
 12 LKISFSLSESLKIKKIPPLIYGLIAGLLEQLERLLIGLRSKGLILIKK 71
 66 IIVSLMLIPPKLISAKLIGIKRPGCVSVVVFYFMYISISLGLITDVRK 125
 72 LVSLSLMLIPPKLISAKLIGIKRPGCVSVVVFYFMYISISLGLITDVRK 131
 126 TTRPKTSNKNLISAKLISVIVWAFPLSLPMMLITNKPDRKVKKCSLEKSEGLV 185
 132 TTRPKTSNKNLISAKLISVIVWAFPLSLPMMLITNKPDRKVKKCSLEKSEGLV 193
 136 WHIVVTVGVFWINELIVVYTHLKEKHSVVRHRCVCKVRKKVAVF11IAVE 245
 192 WSLIVVTVGVFWINELIVVYTHLKEKHSVVRHRCVCKVRKKVAVF11IAVE 251
 246 FTFVVEHARIVYHSDRWVHTAENMLFVYKSTWMLISNACLPD11YFELKCKSP 305
 252 FTFVVEHARIVYHSDRWVHTAENMLFVYKSTWMLISNACLPD11YFELKCKSP 311
 406 FNSLSLSMKPNVATSLSCJNPKRPGVADPN 347
 412 FNSLSLSMKPNVATSLSCJNPKRPGVADPN 348

RESULT 11
 AA004007

ID AA004387 standard; Protein: 267 AA.
 XX
 XX AA004387;
 XX
 XX 04-SEP-2001 (first entry)
 XX
 XX Human P2 purinergic receptor subtype, P2Y12 truncated allelic variant.
 XX
 XX Human; P2-purinergic receptor; P2Y12; variant; vasoregic; thrombolytic;
 XX cerebroprotective; gynecological; ADP; adenosine 5'-diphosphate; angina
 XX myocardial infarction; ischaemic attack; preclampsia; bleeding disorder;
 XX carotid endarterectomy; vascular graft surgery; brain disorder; migraine;
 XX vascular injury; schizophrenia; eating disorder; depression; angioplasty;
 XX peripheral vascular disease; platelet aggregation; restenosis; embolism;
 XX thrombocytopenic purpura; stroke; peritonitis; toxin-sensitive G protein;
 XX G1; disseminated intravascular coagulation; thrombosis; mutant; mutant;
 XX variant.
 XX
 XX Homo sapiens.
 XX
 XX Synthetic.
 XX
 XX W0200146454-A1.
 XX 28-JUN-2001.
 XX
 XX 26-DEC-2000; 2000WO-US34998.
 XX
 XX 23-DEC-1999; 99US-6171622.
 XX
 XX (COPT-) COP THERAPEUTICS INC.
 XX
 XX Conley PB, Janitzen H, Ramakrishnan-Dubridge V, Julius DJ;
 XX Hollinger G;
 XX WPI: 2001-418082/44.
 XX N-PSDB: AAD08700.
 XX
 XX Novel isolated ADP receptor, termed P2Y12 receptor polypeptide, useful
 XX for identifying binding partners and for diagnostic applications
 XX
 XX Claim 29; Page 91 92; 108pp; English.
 XX
 XX The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed
 XX as P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor is
 XX the subtype of P2-purinergic receptor. The P2Y12 receptor is expressed
 XX selectively in the platelets and brain, and couples to a pertussis toxin-
 XX sensitive G protein (G_i). P2Y12 receptor is a G protein-coupled receptor
 XX that responds to ADP. The invention also relates to a method for
 XX identifying an agent which is useful for modulating acute myocardial
 XX infarction, unstable angina, chronic stable angina, transient ischaemic
 XX attacks, strokes, peripheral vascular disease, preclampsia, deep venous
 XX thrombosis, embolism, disseminated intravascular coagulation, thrombotic
 XX thrombocytopenic purpura or a bleeding disorder; thrombotic and
 XX restenotic complications following angioplasty; carotid endarterectomy;
 XX post CABG (coronary artery bypass graft) surgery; vascular graft surgery;
 XX stent placements or insertion of endovascular devices and prostheses.
 XX P2Y12 receptor is useful for identifying binding partners and for
 XX diagnostic applications. P2Y12 receptor provides targets for screening
 XX synthetic small molecules and combinatorial or naturally occurring
 XX compound libraries to regulate platelet aggregation, vascular injury, or
 XX disease as well as schizophrenia, eating disorders, depression, migraine
 XX and other brain disorders. The present sequence is human P2-purinergic
 XX receptor subtype, P2Y12 truncated allelic variant. The variant is
 XX obtained by deleting two bases "CA" from position 789-790 of the wildtype
 XX human P2Y12 receptor cDNA, resulting in amino acid changes from position
 XX 249 of the wildtype human P2Y12 receptor.
 XX
 XX Sequence 267 AA.

Query Match 69.6%; Score 1237.5; DB 22; Length 267;
 Best Local Similarity 95.7%; Pred. No. 9, 4e-128;
 Matches 242; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

QY 1 MGVADNLTISAGNNTSLCTROKKITOVLEPLLYTVLPFVGLITNGLAMPFFQIPKSNFI 60
 DB 1 mgavdhltisagpntslctrdykltcqvllpilyvltfvglitnglamrffqirsksnfi 60
 QY 61 IFLKNTVTSIDLMLITPEFKILSDAKLTGRLRTFVQVTSVFIFPMVVISISFLITL 120
 DB 61 IFLKNTVTSIDLMLITPEFKILSDAKLTGRLRTFVQVTSVFIFPMVVISISFLITL 120
 QY 121 DRYQKTRTPKTSNKNLGAALISVIMAPMPLISLPMILINROPRDNKVKCSFLKS 180
 DB 121 drryqktrtpktsnknlgaaalissvimapmplislpmlilnrpdrdnvkcsflks 180
 QY 181 EFGLEWHEIVNYICGVIFMINEIVTVVYTLITRELYRSVPTGSKVKPKKYNKVF 240
 DB 181 efglewheivnyicgvifmifvnyvtylitrkelyrsvptgskvkpkkynkvfy 240
 QY 241 IIAVETI-CFVFF 252
 DB 241 hecllyllesdpl 253

RESULT 12

ID AAB23029 standard; Protein: 333 AA

AC AAB23029;

DT 16-JAN-2001 (first entry)

DE Human chemokine receptor-like protein, SECX 2777610.

XX SECX protein; human; secreted; membrane-associated; cancer;
 XX proliferation regulator; differentiation regulator; non-malignant tumour;
 XX immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;
 XX infection; inflammatory disorder; arthritis; haematopoietic disorder;
 XX skin disorder; cardiovascular disorder; atherosclerosis; restenosis;
 XX neurological disease; Alzheimer's disease; trauma; wounding;
 XX spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;
 XX anti-HIV; antiinflammatory; antiarthritic; antileukosclerotic;
 XX neuroprotective; vintory; antiallergic; antitubercular; cardiac;
 XX dermatological; gene therapy.

XX Homo sapiens.

XX W0200053742-A2.

XX 14-SEP-2000.

XX 09-MAR-2000; 2000W-11S05280.

XX 09-MAR-1999; 9905-0123667.

XX 08-MAR-2000; 2000US-0123667.

XX (CURA-) CURAGEN CORP.

XX Shimkels RA;

XX WPI; 2000-594318/56.

XX N-PSDB; AAA93616.

XX Novel human membrane associated or secreted polypeptides and
 XX polynucleotides useful for diagnosis, prevention and treatment of
 XX pathological states such as cancer, immune, cardiovascular and
 XX neurological disorders.

XX Claim 1: Fig 1: 151pp; English.

XX Sequences AAB23029-823048 represent human SECX proteins. The SECX
 XX proteins of the invention are either secreted or membrane-associated
 XX and act as regulator of cellular proliferation and
 XX differentiation. SECX proteins or nucleotides are useful for diagnosing
 XX the presence of, or predisposition to, a disease associated with altered

CC levels of SECX proteins and nucleotides. The SECX proteins are also
 CC useful to screen compounds that modulate SECX activity or expression. The
 CC interaction of a SECX protein with other cellular proteins may be useful
 CC to modulate the activity of a partner protein. SECX nucleotides are useful
 CC for the recombinant expression of SECX protein, and may be used to detect
 CC SECX mRNA or genetic lesions in the SECX gene. They may also be used to
 CC modulate SECX expression (e.g., using antisense oligonucleotides). SECX
 CC nucleic acid sequences are also useful for identifying a cell or tissue
 CC type in a biological sample, and in forensic biology. SECX primers or
 CC probes are useful for detecting the presence of SECX nucleotides and for
 CC screening tissue cultures for contamination. Diseases that may be treated
 CC or prevented using SECX proteins or nucleotides include cancer (e.g.,
 CC colorectal carcinoma, prostate cancer), benign tumours, immune disorders
 CC (including autoimmune diseases, transplant rejection, allergies, AIDS),
 CC infections, inflammatory disorders, arthritis, haematopoietic disorders,
 CC skin disorders, cardiovascular disorders, Alzheimer's disease, trauma (e.g.,
 CC neurological diseases (e.g., Alzheimer's disease), atherosclerosis, restenosis,
 CC surgical or traumatic wounds, spinal cord injury), and skeletal
 CC disorders.

SO Sequence 333 AA;

Query Match 46.6%, Score 829; DB 21; Length 333.
 Best Local Similarity 49.1%, Fred. No. 11e-82;
 Matches 155; Conservative 57; Mismatches 102; Indels 2; Gaps 1;

QY 17 CPMDYKLTQVLEPLLYTVLPFVGLITNGLAMPFFQIPKSNFIPLKNVISHLMLIT 76
 DB 15 cpmdyltqvlepllytvlpfvglltnglamrffqirsksnfllpknvishlmlit 74
 QY 77 FPKKILSDAKLTGRLRTFVQVTSVFIFPMVVISISFLITLDRYQKTRTPKTSNPK 136
 DB 75 fpkkilsdshlpgwqlratvctfsvtycmtygvilgllafdrfkilrprnrfik 134
 QY 137 NLGAKLTSLVIAFELLISLPMILINROPRDNKVKCSFLKSEFGVMEIVNYICGV 196
 DB 135 kpylakvstfifwiflffislpmlismkcaatpsvkkrcasikpgjlkwhgmynctgf 194
 QY 197 IPWIMPLIVVCYTLITRELYRSVPTGSKVKPKKYNKVFIIIAVETICFVFFHRA 256
 DB 195 ifwvimlilvifvnyvtylitrkelyrsvptgskvkpkkynkvfyiiaavetifvffh 254
 QY 257 IPRYLSOTRQVPCOTANLTFYKPSLMTSLNACIDPFIYFPLKSPRNSLSMLKCP 316
 DB 255 vpyhsqtmktucriqnyqfifakeltllflaatnctmcp; i; y; f; i; c; k; k; t; c; k; p; e; m; y; -; g; 312
 QY 317 NSATSLSQDNKKKEQD 332
 DB 313 fkltsaqdnkssqtd 328

RESULT 13

ID AAB74397 standard; Protein: 333 AA.

AC AAB74397;

DT 11-JUL-2001 (first entry)

DE Human G protein coupling receptor.

XX Human; G protein coupling receptor; CNS; central nervous system.

XX Homo sapiens.

XX JP2001054389-A.

XX 27-FEB-2001.

XX 17-AUG-1999; 99JP-0230777.

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 FT /note= "First EC loop"
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 FT /label= Transmembrane_domain_(31M)
 FT 119..135
 FT /label= Intracellular_domain
 FT /note= "Second IC loop"
 FT 136..160
 FT /label= Transmembrane_domain_(41M)
 FT 161..188
 FT /label= Extracellular_domain
 FT /note= "Second EC loop"
 FT 189..211
 FT /label= Transmembrane_domain_(51M)
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 FT /label= Transmembrane_domain_(61M)
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